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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Command line parameters:

-MODEL-frame+ p2n.model -DEV=xlh
-O_-(Ggn2_1/USPTO_Spool_h/US10627571/runat_27072005_154720_27503/app_query.fasta_1.327
-OB=GenEmb1 -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -EMD=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DCCALIGN=200 -THR_SCORE=pct -THR_MAXILO -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10627571 @CGN 1 1 3731 @runat 27072005 154720 27503 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPEJOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum
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Maximum Match 100%
Listing first 100 summaries
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Perfect score:
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                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                Score
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seq length: 2000000000
                                                                              Query
Match
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Ygapop 10.0 , y
Fgapop 6.0 , F
Delop 6.0 , D
                                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl: *
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Submitted (05-JUN-1998) Biochemistry, Academic Media
Submitted (15 Ameterdam 1105 AZ, The Netherlands
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Location/Qualifiers
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Horrevoets, A.J., Fontijn, R.D., van Zonneveld, A.J., de Vries, C.J.,
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Horrevoets, A.J.G., Fontijn, R.D. and Pannekoek, H.
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Best Local Similarity:
Query Match:
DB:
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  Eukaryyta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1921)

E 0ta, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.,
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11723 09-JUL-2002;

HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN D2002191363-A/11723
PD 09-JUL-2000
PF 208-JUL-2000
PF 208-JUL-2000 JP 2000280990
PF 28-JUL-2000 JP 2000280990
PF 28-JUL-2000 JP 2000280990
PT TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
PI SAITO,
PI JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
PI KEIICHI NAGAI, TETSUJI OTSUKI
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JP 2002191363-A/11723.
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JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU
KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                              09-JUL-2002
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TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
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/mol_type="genomic DNA"
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 12751 07-FEB-2001;
Research Association for Biotechnology (JP)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                       Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarau; Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ishii,S., Kawai,Y., Saito,X., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki,N.
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AK001931 GI:7023502
Oligo capping; fis (full insert sequence)
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human cDNAs
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human cDNA sequencing project
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                       location/Qualifiers
                                                                                                                                                                                               Tokyo.
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., Nagai,K., Kimura,K., Makita,H.,
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highly similar
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REFERENCE
AUTHORS
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ORGANISM
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Best Local Similarity:
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                                                                                                                                                                                    VERSION
                                                                                                                                                                                                       ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40
           Eukaryota; Metazoa; Chordata; Craniata; Verteb Mammalia; Eutheria; Primates; Catarrhini; Homi 1 (bases 1 to 573)
Ebert, L., Schick, M., Neubert, P., Schatten, R., Cloning of human full open reading frames in Gentry vector (pDONR201)
                                                                                                                                                                                                   Homo sapiens full open reading frame CDNA clone RZPDo834H12 gene TWFAIP8, tumor necrosis factor, alpha-induced protein complete cds, incl. stopcodon.

CR457137
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entry vector
Unpublished
                                                                                                                             Homo sapiens (human)
                                                                                                                                                               CR457137.1 GI:48146390 Full ORF shuttle clone,
                                                                                                                                                                                                                                                                                                                                                                      LysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                           TTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
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/clone_lib="pLACE1"
/note="cloning vector: pME18SFL3"
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954.00
99.47%
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                                                                                           Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae;
                                                                                                                                                               Gateway (TM), complete cds
                                                                                                                                                                                                                                                                           573 bp
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                                                                                                                                                                                                                                                        p mRNA linear PRI 03-JUN-200
frame cDNA clone RZPDo834H127D for
                                                                                           Hominidae;
                                                       Henze, S. and
                                                                                           Euteleostomi; Homo.
                                                                                                                                                                                                                                                                           PRI 03-JUN-2004
                                                       Korn, B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
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:
                                                                                                                                                                                          Match:
                   67
                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide.
The stop codon has been set to TAA followed by
TTAACCCAGCTTTCTT. .att. Compared to the reference sequence NM_014350
we did not find any amino acid exchanges.
Clone distribution: http://www.rzpd.de/products/orfclones/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contact RZPD (customer service@rzpd.de) for further informati This CDS clone is a part of a collection of human full length expression clones generated by RZPD.

This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the codon: att. AAAAAA GCA (GGC (ATG)).

The last base of the last coding triplett has been changed to which might lead to an amino acid change at the C terminus of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Germany
RZPD; RZPD0834H127D, ORFNO 1910
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834H127D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (03-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ebert, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone is available from RZPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www.rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: +49 30 32639 100 Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www.rzpd.de/products/orfclones/
Contact: Inge Arlart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomitorschung GmbH,
                                   GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                    MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                 GGTAAAATGGTGTCCAAATCCATCGCCACCATCATAGACGACACAAGTAGTGAGGTG
                                                                             GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 573)
ert,L., Schick,M., Neubert,P., Schatten,R., Henze,S.
                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="TNFAIP8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone lib="Human Full ORF Clones Gateway(TM) -
'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                            gene="TNFAIP8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone="RZPDo834H127D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pDONR201, Site_1: attP1; Site_2:
                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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181 LysMetLeuAspGluGluAsnIle 188
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                                                                                                                                     PC C12P21/02,C12V1/00// ....Primer for synthesizing full-length Location/Qualifiers (71). (664).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1729)
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JP 2002191363-A/11628.
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KEIICHI NAGAI,TETSUJI OTSUKI
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TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                         Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Ocsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 12578 07-PEB-2001; Research Association for Biotechnology (JP) Location/Qualifiers 1. 1729
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Sequence 12578 from Pate
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                           /organism="Homo sapiens"
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                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
Ota,T., Suzuki,Y., Nishikawa,T., Ot
Wakamatsu,A., Hayashi,K., Sato,H.,
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HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                            Homo sap
AK001850
AK001850.1 GI:7023373
Oligo capping; fis (full
Homo sapiens (human)
                                                                                         AK001850
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                                                                                                                                                                                                MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
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                                                                                                                                          AAAATGTTGGATGAAGAGAACATA
                                                                                                                                                                                                                                                                       SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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                                                                                                                                                                                                                                                                                                               CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
                                                                         sapiens
                                                         0 1729 bp mRNA linear piens cDNA FLJ10988 fis, clone PLACE1001920, sapiens MDC-3.13 isoform 2 mRNA.
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950.00
99.47%
98.94%
98.75%
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Matches:
Conservative:
Mismatches:
Indels:
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                    sequence)
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186
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highly similar
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Otsuki,T., .

Sugiyama,T.,
Kimura,K.,

Makita, H.,

'n

Hominidae;

Euteleostomi;

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TITLE
JOURNAL
REFERENCE
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AUTHORS
                                                                          Best Local Similarity:
Query Match:
DB:
US-10-627-571-2 (1-188)
                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                 Alignment Scores:
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TITLE
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Kumagai, A., Takura, S., Fukuzumi, Y., Fujinori, Y., Komiyama, M.,
Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y.,
Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N.,
Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Noguchi, S., Itoh, T., Shigeta, K., Senba, T., Matsumura, K.,
Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T.,
Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J.,
Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K.,
Nagase, T., Nomura, N., Kikuchi, H., Masuho, Y., Yamashita, R.,
Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
Complete sequencing and characterization of 21,243 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Takahashi-Pujii, A., Hara, H., Tanase, T., Nomura, Y., Togiya, S., Komai, F., Hara, R., Takeuchi, K., Arita, M., Nabekura, T., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahari, K., Masuho, Y. and Oshima, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Isogai, T. and Otsuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NEDO human cDNA sequencing project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
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x AK001850 (1-1729)
                                                                          1.89e-75
950.00
99.47%
98.94%
98.75%
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Matches:
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186
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                                TITLE
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             RS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, X.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and mouse CNNA semence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1814)

1 Grouse L.H., Derge, J.G.,
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:::|
human and mouse cDNA sequences
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1814 bp mRNA linear PRI 24
Homo sapiens tumor necrosis factor, alpha-induced protein
(cDNA clone MGC:12451 IMAGE:3997650), complete cds.
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      174
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (27-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
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                    MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
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DTSSEVLDELYRVTREYTQNKKBAEKIIKNLIKTVIKLAILYRNIOPNODELALMEKF
KKKVHQLAMTVVSFHOVDYTFDRNVLSRLLNECCEMLHQIIQRHLTAKSHGRVNNVFD
HESDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
                                                                                                                                                                                                                                                                                                 (DUF758). Family of eukaryotic function, which are induced by /db_xref="CDD:pfam05527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="TNFAIP8 protein"
/protein_id="AAH05352.1"
/db_xref="GI:13529164"
                                                                                                                                                                                                                                                                                                                                                           note="DUF758; Region: Domain of unknown
                                                                                                                                                                                                                                                                                                                                                                                /gene="TNFAIP8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="LocusID:25816"
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/tlssue_type="Bladder, carcinoma"
/clone_lib="NIH_MGC_53"
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; C
Mammalia; Eutheria; Primates; C
1 (bases 1 to 1915)
Nietfeld, W. and Meyerhans, A.F.
Identification of cellular fact
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                                                                                                                                                                                                                     2 (bases 1 to 1915)
Nietfeld,W. and Meyerhans,A.F.
Direct Submission
Submitted (13-OCT-1998) Max Planck Institute for Molecular Genetics, Ihnesstrasse 73, Berlin 14195, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens MDC-3.13 isoform AF099935 AF099935.1 GI:3860092
                                                                                                                                                                                                                                                                                                                               of dendritic cells
                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Query DB:

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                                                       Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and oth
                                                                                                                 Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                Patent: WO 02068579-A 12009 06-SEP-2002; PE Corporation (NY) (US)
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                                 Mammalla; Butheria; Primates; Catarrhini; Hominidae; Locales to 2003)

Nietfeld, W. and Meyerhans, A.F.

Identification of cellular factors involved in the of factoric calls.
of dendritic cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nietfeld, W. and Meyerhans, A.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                            ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
                                                                                                     LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
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                                                                                                                                                                                                                                                                                                                                                           TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
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                                                                                                                                                     TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
                                                                                                                                                                                                                                                                                          ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTTGACCGGAATGTGTTATCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="mavatdvensknilavqaqkkilgknvsksiattliddtssevld
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
B
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98.75%
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BC007014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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                                 gene
                                                                                                                                                                                      source
                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: b Column: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 765712:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg, R.
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matched mRNA gi: 7657123

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Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Worley, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCUU/V114 2081 bp mRNA linear PRI 24-FBB-20V
Homo sapiens tumor necrosis factor, alpha-induced protein 8, mRNA (CDNA clone MGC:12346 IMAGE:3930240), complete cds.
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                         Α.,
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                                                                                                                                            LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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function, which are induced by tumour necrosis factor"
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65348
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ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
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8 밁 Ś 밁 Ś 밁 Ş 뮹 S

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Percent Similarity:
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                                                                                                                                                                        61 LysIleLysAsnLeuIleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGln
                                                                                                                                                                                                                                                                                                                                                    21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                                                                                                                                                                                                           www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
STS Content:
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On Apr 27, 2001 this sequence version replaced gi:7712094
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DOE Joint Genome Institute.
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DOE Joint Genome Institute and Stanford Human
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MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                    PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
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/chromosome="5"
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Best Local Similarity:
Query Match:
DB:
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Quality: Phrap Quality
Estimated Total Number
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On Sep 21, 2001 this sequence version replaced gi:15383783
Draft Sequence Produced by DOE Joint Genome Institute
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Submitted (24-MAR-2000) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
3 (bases 1 to 156277)
DOE Joint Genome Institute and Stanford Human Genome Cer
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Finishing Completed at Stanford Human Genome Center
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Submitted (21-SEP-2001) DOE Joint Genome Institute,
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4 (bases 1 to 156277)
DOE Joint Genome Institute and Stanford Human Genome Center.
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1 (bases 1 to 156277)
DOE Joint Genome Institute and
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DOE Joint Genome Institute.
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 158057)
Sulston, J.E. and Wilson, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
Wilson,R.
Direct Submission
Submitted (30-MAY-2003)
                                                                                                       Direct Submission
Submitted (11-JAN-2003) Genome
University School of Medicine,
                                                                                                                                                                         3 (bases 1 to 158057)
Waterston, R.H.
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Tomlinson,C. and Bielicki,L.
The sequence of Homo sapiens
Unpublished (2001)
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Department of Genetics, Washington

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FEATURES
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Clone CTD-2293E22 is from a release of the human BAC library CT
The library contains cloned DNA from human sperm. See: Shizuya
al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et a
Genomics 34:213-8 (1996). The close is available from Research
Genetics, Inc. (http://www.resgen.com).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
------- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUCSC
Web site: http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_MS2293E22
                      /rpt_family="L1" 5767. .6328
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27433. .28325
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21591. .22250
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24487. .24515
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|9548. .19664
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|5273. .15541
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[4630. .14899
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HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002508167-A/107
PR 18-DEC-1997 US 60/068 0057,18-DEC-1997 US 60/068 007 PR
18-DEC-1997 US 60/068 0057,18-DEC-1997 US 60/068 054 PR
18-DEC-1997 US 60/068 064,18-DEC-1997 US 60/068 053 PR
18-DEC-1997 US 60/068 169,19-DEC-1997 US 60/068 054 PR
19-DEC-1997 US 60/068 367,19-DEC-1997 US 60/068 369 PR
19-DEC-1997 US 6
                                                                                                                      Similarity:
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1 (bases 1 to 1943)

Moore, P.A., Ruben, S.M., Carter, K.C., Shi, Y., Rosen, C.A.,

Soppet, D.R., Caou, H., Wei, Y.F., Florence, K., Duan, R.D.,

Florence, C., Greene, J.M., Feng, P., Ferrie, A.M., Yu, G.L., Janat, F.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Salto,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yamamoto,J., Salto,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Yamurakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Puruya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Pujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sato,S., Moniya,S., Moniyana,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,
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Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                           21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40
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                                                                                                                                                                                                                                                     Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamateari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kanehori,K., Ishibashi,T., Chiba,Y., Fujimori,K., Hiraoka,S., Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Hotute,T., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishi,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

Location/Qualifiers
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Isogai, T. and Yamamoto, J.
Direct Submission
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="spleen"
/clone_lib="SPLEN2"
/note="cloning vector:
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,
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Mus musculus
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1728)
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                               Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BC009090.1 GI:14318585
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 195: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Life Technologies, I
cDNA Library Arrayed by: The I.M.A.G.E. Conso
DNA Sequencing by: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contect: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
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LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln 80
                                                                                                  LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                                                                                                                                                            MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
:::
                                                                                                                                                                         GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCGAGGTG
                                                                                                                                                                                                    GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                                                 GTGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
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KKKVHQLAMTVVSFHQVEYTFDRNVLSRLLNECRELLHEIIQRHLTAKSHGRVNNVFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam1" /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="Tnfaip8"
/note="synonyms: Nded, Gg2-1, Ssc-2"
/db xref="LocusID:106869"
/db xref="MGI:2147191"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HFSDCDFLAALYNPFGKFKPHLQKLCDGINKMLDEENI"
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="MGC:11714 IMAGE:3965693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="TNF-induced
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="Infaip8"
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920.00
98.94%
94.15%
95.63%
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Indels:
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GTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAG

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REFERENCE
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AUTHORS
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SOURCE
ORGANISM
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ACCESSION
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                                                                                                                                                                                                                                                 RS Birren, B. Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barma, N., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farroira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gilnde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Indblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Ngyen, C., Nicol, R., Morbu, C., Norman, C.I., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Wargh, P., Pierre, N., Pollara, V., Nurbu, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ve, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          520
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        Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 184327)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V.,
Bloom, T., Boguslavki, L., Boukhgalter, B., Camarata, J., Chang, J.
Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B.,
DeArtellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L.,
Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
Anderson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
Brickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D.,
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Mus musculus
Mus musculus
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Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                    Submitted (13-MAY-2002) Whitehead Institute/MIT Center
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AC120859.12 GI:50979395
  Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus chromosome 18, clone RP24-200D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus chromosome 18, clone RP24-200D2, complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LysMetLeuAspGluGluAsnIle 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGGCATCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGATTGTGATTTTTTGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 184327)
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                                                                                                   Camarata, J., Chang, J.,
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, Dorris,L.,
,M., Gage,D.,
re,N., Hafez,N.,
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repeat_region
                                                repeat_region
                                                                                                                                                                                                      misc_feature
                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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4 (bases 1 to 184327)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@broad.mit.edu

------- Project Information

Center project name: L1053

Center clone name: 200_D_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
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3199. .. 3484
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site:MboI"
                                                                   /rpt_family="AT_rich"
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/clone_lib="RPCI-24 Male Mouse BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                               map="18"
                                                                                                                                                                                                                                                                                                            /chromosome="18"
                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA
/db_xref="taxon:10090"
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Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M. Hall, J., Horton, L., Hulme, W., Iliev, I.,

Direct Submission
Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chaegel, Y., Collymore, A., Cooke, P., Coorum, B., Chaegel, Y., Collymore, A., Cooke, P., Coorum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farzo, S., Ferreira, P., FitzGerald, M., Gage, D., Erickson, J., Farzo, S., Graham, L., Grand-Pierre, N., Hafez, N., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., MacChan, C., MacChan, C., Madord, P., Major, J., Mamming, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassilev, H., Venkataraman, V. S., Viel, R., Vu, M., Milson, B., Mu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Submitted (Na. Altr., 2004) Whitehead Institute/MT Center for Genome

Submitted (05-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 5, 2004 this sequence version replaced gi:49035085.

Center: Whitehead Institute/MIT Center for Genome Research

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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                          Rattus norvegicus clone CH230-10A12,
1 (bases 1 to 237561)
Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
                                                               Rattus.
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/rpt family="MTC"
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Adams, C., Alder, J.,

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Davila, M.L., Davis, C., Davy, C., Coyle, M., Cree, A., Davila, M.L., Davis, C., Davy, C., Coyle, M., Cree, A., Dederich, D., Davis, C., Davy, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Bayes, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garcia, A., Garra, M., Guerra, W., Gunaratne, P., Hasland, W., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Jacob, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Johnson, R., Johnson, A., Hogles, M., Hollins, B., Howells, S., Hladtin, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hune, J., Idlebird, D., Jackson, A., Jacob, L., Jacob, L., Jang, H., Johnson, B., Johnson, R., Johnson, R
Submitted (09-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 9, 2002 this sequence version replaced gi:23264563.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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             21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 40
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Best Local Similarity:
Query Match:
                                                                                     US-10-627-571-2 (1-188) x AC095257 (1-237561)
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence will be replaced by the finished sequence as soon as it is available and
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1 237561: contig of 237561 bp
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Center clone name: CH230-10A12
Center clone name: CH230-10A12
Center clone name: CH230-10A12
Assembly program: Phrap; version 0.990329
Consensus quality: 229749 bases at least Q40
Consensus quality: 231209 bases at least Q30
Consensus quality: 231203 bases at least Q20
Estimated insert size: 232575; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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PD 09-JUL-2002
PF 28-JUL-2000 JP 2000280990
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PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Patimer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 4238 09-JUL-2002;
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   /organism="Homo sapiens"
/mol_type="genomic DNA"
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                                                                                                                Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto, Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 4238 07-FEB-2001; Research Association for Biotechnology (JP)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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     ratuwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M., Placihy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M. Full-length cDNAs from bursal lymphocytes to facilitate gene function analysis
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                                                                                                           Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                 LysMet--LeuAspGluGluAsnIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                 SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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Submitted (20 MAY-2004) Caldwell R.B., GSF
Institut fuer Molekulare Strahlenbiologie,
1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caldwell, R.B
              CTGTTGAATGACTGTAGAGAGCTGCTTCATCAGATCATTCAGCGTCACCTAACTGCGAAA
                            LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                    AAGACGGTGGTCAGTTTCCATCAGGTGGATTATACCTTTTGACAGGAATTTCTTGTCCAAA
                                                                                  MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                                       PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
                                                                                                                                                                                   ATCATTAAAAACCTCATTAAAAATAGTCCTCAAATTGGCAATTCTCTACAGGAACAATCAA
                                                                                                                                                                                                  LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
                                                                                                                                                                                                                                                         LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
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/product="hypothetical protein"
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YRVTKEYTQNKKEAEKIIKNLIKIVLKLAILYRNNQFNQDEIALMEKFKKKVHQLAKT
VVSFHQVDYTFDRNFLSKLLNDCRELLHQIIQRHLTAKSHGRVNNVFDHFSDCEFLAA
LYNPFGPYKLHLQKLCDGVNRMLDEGNI"
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/locus_tag="RCJMB04_29h8"
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1. .2009
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/clone_lib="riken1"
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                                                                                                                                                  Oshima, A., Takahashi-Fujii, A., Tanase, T., Imose, N., Takeuchi, K., Arita, M., Musashino, K., Yuuki, H., Hara, H., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamateu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Skitne, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K.
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Isogai, T. and Yamamoto, J.
Direct Submission
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                 nLysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                                                                     gLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLy
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  CAAAATGTTGGATGAAGAGAACATA
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/clone_lib="THYMU2"
/note="cloning_vector
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYMU2004688"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (15-SEP-2004) Sanger Institute, Hinxton, Cambridgeshi CB10 18A, UK. E-mail enquiries: trop@sanger.ac.uk Sanger Xenopus tropicalis EST/CDNA project.

This sequence is from a Xenopus Gene Collection (XGC) library, a library constructed by Aaron M. Zorn. cDNA was prepared from extracted from eggs. EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Kenopus; Silurana.
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                                                      ArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAla 139
                                                                                                                                                                                                                           CAGTTTAATGAGGAAGATTGCACTCATGGAGAAGTTCAAGAGAAAGGTCCATCAGCTG
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/db xref="taxon:8364"
/clone="TBgg053008"
/clone_lib="xGC-egg"
/dev_stage="egg"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                                     Direct Submission
Direct Submission
Submitted (07-JUN-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1193 bp
Xenopus laevis MGC80354 protein,
IMAGE:5074412), complete cds.
BC072904
                                                                                                                                                                                                                      NIH-MGC Project
Contact: XGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein,S.L., Strausberg,R.L., Wagner,L.,
and Richardson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 1193)
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BC072904.1 GI:49115085
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                 Klein, S. and Gerhard, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic and genomic tools for Xenopus
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                                                 info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               initiative
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                                                                                                                                                                                                 cgapbs-r@mail.nih.gov
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mRNA (cDNA clone MGC:80354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      research: The NIH Xenopus
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Clifton, S.W

VRT 03-AUG-2004

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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 152 Row: j Column: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Li Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mori Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                  AlaMetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSer 119
                                                                                                                                                                                                                            GlnPheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeu
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/product=_idmGR0354 protein"
/product_idmGR0354 protein"
/protein_idmCR0354 protein"
/db_xref="GI:49115086"
/db_xref="GI:4
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/db_xref="taxon:8355"
/clone="MGC:80354 IMAGE:5074412"
/clone="MGC:00354 IMAGE:5074412"
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/db_xref="LocusID:443963"
153. .722
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/clone_lib="NICHD_XGC_Ov1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Xenopus laevis"
/mol_type="mRNA"
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Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

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JOURNAL
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REFERENCE
AUTHORS
TITLE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetcw, K.H., Schaefer, C.F., Bhat, N.K.,

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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

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     Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
CDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kar
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anurad
                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (23-MAY-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidormes; Cyprinidae; Danio.

1 (bases 1 to 3986)
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Danio rerio
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(cDNA clone
                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3986)
Director MGC Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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Stephanie Rodrigues, Amy Sanchez
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Mark Ketteman,
and Michelle W
Michelle Whiting
                                Anuradha
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Best Local Similarity:
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                                                                                                               GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSorHisGly 143
                                                                                                                                                                                                                                                                                                AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGlu
                                 ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn 163
                                                                                                                                                                                                           ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn 123
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                                                                                            GACTGCCGTGAACTTCTGCACCAGGCCATCAATCGGCATCTAACGGCGAAATCTCACGCC 618
                                                                                                                                                                                 GTTAGCTTCTACCAGATCGACTTCACTTTTGATCGACGCGTCATGAGTAATCTACTCAAT
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CGAATCAACCATGTCTTCAATCATTTCGCCGATTGTGACTTCCTCGCGACGCTATACGGA 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGTACAGAGTCACCAAAGAGTACACGCGCAACGCGAAGGGCCCCAGAAGATCATCAAA
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lone was selected for full length sequencing because it
the following selection criteria: matched mRNA gi: 41056158.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="mdsfstknlalqaqkklmskmatktvanlfiddtssevldelyr
vtkbytrnrkeaqkiiknlikmvvklgvlyrngqfnnselalverfrkkvhtlamtav
sfyqidftfdrrvmsnllndcrellhqainrhltaksharinhvfnhfadcdflatly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="Whole body, adult, (one male including unfertilized eggs)"
(clone lib="Sugamo Kawakami zebrafish DRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="tumor necrosis factor, alpha-induced
/protein_id="AAH52765.1"
/db_xref="GI:31127058"
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'db_xref="LocusID:393303"
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                         During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest road mality representation will be here
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-FEB-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 6, 2004 this sequence version replaced gi:41392451.
                                                                                                                                                                                                                                          discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see
                                                                                                                                                                                                                                                                                         Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                      http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEY-49M19
is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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205949 bp DNA linear VRT 06-FEE Zebrafish DNA sequence from clone DKEY-49M19 in linkage group
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                                                                                                                                                                                 pIndigoBAC-5
                                                           /db_xref="taxon:7955"
                       /clone="DKEY-49M19"
/clone_lib="DanioKey"
                                                                                                        organism="Danio rerio"
                                                                                                                                                            location/Qualifiers
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Gallus gallus
Gallus gallus
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Eukaryota; Meognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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   2 (bases 1 to 1589)
Caldwell,R.B.
Direct Submission
                                                                            Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezz
Fiedler,P., Kutter,S., Blagodatski,A., Kostov
Plachy,J., Carninci,P., Hayashizaki,Y. and Bu
Full-length cDNAs from bursal lymphocytes to
                                                Unpublished
                                                                 function analysis
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1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
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                                                                                                                                                                           GAGGAGCTGCTGGTGATGGAGCGCTTCCGCAAGAAGGTGCACACCTTGGCCATGACAGCG
                                                                                                                                                                                                                                                                                                                                                                   GCATCCAAGACAGTGGCCAATGTCTTCATTGATGACACAAGCAGCGAGATCTTGGATGAG
ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn|||:::||||:::|||||||||||
                                                                                                                                                                                         AspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrVal 103
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                                                  GAGTGCCGGGACCTCCTGCACCAGGCTGTCAGCAGCCACCTGACGGCCAAGTCACACTCC
                                                                    GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
                                                                                                             GTGAGCTTCCACCAGATAGACTTTACGTTTGACCGCAGGGTCGTGTCAAGTGTGCTGACA
                                                                                                                             ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn
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/db_xref="GI:59113332"
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SFHQIDFTFDRRVVSSVLTECRDLLHQAVSSHLTAKSHSRINHVFNHFADYEFLSALY
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/clone_lib="riken1"
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CQ736656
CQ736656.1 GI:42332642
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                          ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn
                                                                                          GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
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/mol_type="unassigned DNJ
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Yamamoto,J., Isono,Y., Nagai,K. and Iri
Full-length human cdna
Patent: EP 1440981-A 269 28-JUL-2004;
Research Association for Biotechnology
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                   GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
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/mol_type="unassigned DNI
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                                                                                                                                                      /codon_start=1
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/protein_id="BAC85572.1"
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/db_xref="GI:34528785"
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VIVEKFRKKLNQTAMTIVSFYEVEYTFDRNVLSNLLHECKDLVHELVQRHLTPRTHGR
INHVENHFADVEFLSTLYSLDGDCRPNLKRICEGINKLLDEKVL"
                                                                                                                                                                                                                                                                                                                                              note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                               /note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="amygdala"
/clone_lib="BRAMY2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="BRAMY2038484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
1.04e-48
651.00
89.07%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _type="mRNA"
Length:
Matches:
Conservative:
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REFERENCE
AUTHORS
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AC012678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188937 bp DNA 1.
Homo sapiens chromosome 15 clone RP11-394B5,
SEQUENCE, 10 unordered pieces.
AC012678
                                                                                                                              2 (bases 1 to 188937)
Bruno, D., Conn.E., Dela Rosa, M., Federspiel, N., Foreman, P.,
Bruno, D., Conn.E., Lela Rosa, M., Mao, J., Marathe, R.,
Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R.,
Morehouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J.,
                                                                                                                                                                                                                                                               Bruno, D., Conn, L., Dela Rosa, M., Federspiel, N., Foreman, P., Glukhov, S., Hansen, N., Hyman, R., Mao, J., Marathe, R., Morebouse, A.J., Oefner, P., Palm, C.J., Ramirez, D., Wilhelmy, J., Yu, S., and Davis, R.W.
                        Submitted (03-NOV-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 943
                                                                            Direct Submission
                                                                                                          Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1; HT
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGCAT
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                                                                                      US-10-627-571-2 (1-188) x AC012678
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Best Local Similarity:
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                                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                           Alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                       GATGTTTTTAGTTCAAAGAGTCTTGCGCTTCAAGCCCAGAAGAAGATTCTGAGCAAAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 185828; agarose-fp
Insert size: 188487; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; agarose-fp
Quality coverage: 5.2 in Q20 bases; sum-of-contigs.
NOTE: This is a 'working draft' sequence. It currently
consists of 10 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                        AspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jan
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15973
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26920
39747
39797
54670
54720
69898
69898
69946
93526
138959
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Chemistry: Dye primer; 0% of reads
Chemistry: Big Dye Terminator; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 177081 bases at least Q30
Consensus quality: 18532 bases at least Q30
Consensus quality: 186766 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: 698
Center clone name: RP11-394B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Stanford DNA Sequencing and Technology Development
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2221
7219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21, 2000 this sequence version replaced gi:6223629.
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                                                                                                                                                                                                                                                                                                                                                                                                  Location,
                                                                                                                                                                                                                                                                         /clone="RP11-394B5"
/clone_lib="RPCI human BAC library 11"
                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                           7268: gap of unknown length
15972: contig of 8654 bp in length
15972: gap of unknown length
26869: contig of 10897 bp in length
26919: gap of unknown length
39746: contig of 12827 bp in length
39796: gap of unknown length
39796: gap of unknown length
54669: contig of 14873 bp in length
54719: gap of unknown length
54719: contig of 23528 bp in length
54719: contig of 45433 bp in length
54719: contig of 45433 bp in length
138958: contig of 49929 bp in length
18937: contig of 49929 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                              /Qualifiers
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gap of
contig
                                                                                      (1-188937)
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ig of 4998 bp in length
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Matches:
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AUTHORS
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51934 GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
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                                                                                                                           Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Nesbitt,R., Traicoff,R. and Hood,L.
                                                                                                                                                                                                                            Submitted (08-JUL-2000) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
                                                                                                                                                                                                                                                                                                                             Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T. and Hood, L.
                                           Submitted (23-FEB-2001) Multimegabase Sequencing Center, Instit for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 189796)
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Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G.,
Nesbitt,R., Traicoff,R. and Hood,L.
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Percent Similarity:
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    GCCAGCAAAACTGTGGCCAACATGTTGATGATGACACCAGCAGCGAGATCTTTGATGAG
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                                                                                              GACTTAATCAAGGTGGCGATCAAAATCGGGATCCTCTACCGGAACAACCAGTTTAGCCAA
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Contact: leerowen@systemsbiology.org
Drafting center: SDSTDC
------ Summary Statistics
Sequencing vector: pUC18; LD8752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
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/clone lib="RPCI human BAC library 11"
/clone lib="RPCI human BAC library 11"
/note="Data from overlapping BACs RP11-105D1 and
RP11-52C320 were added and the consensus sequence
determined from RP11-394B5 to the extent possible"
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104690. .104715
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Continuation (2 of
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                            145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
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ValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnPro
                                                                                                                                                                                                                                                    ValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetVal 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCCCAGGACCCACGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                           TACAAAGTCACCGAAGAACACCCACAACAAGAAGGAGGCCCACAAGATCATGAAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsn 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu 183
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                                                                                                CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg 144
                                                                                                                                                               AGCTTCTACGAAGTGGAGTATACCTTTGATACGAATGTGCTCTCTAAACTTCTGCATGAG
                                                                                                                                                                                       SerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGlu 124
                                                                                                                                                                                                                                                                                              GluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValVal 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAAAACTGTGGCCAACATGCTGATCGATGACACCAGCGAGATCTTTGATGAGCTG
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Cheveland, C., Cockrell, R., Cox.C., Coyle, M., Cree, A., D'Souza, L.,
Delgado, O., Denson, S., Darvy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Dinp, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dumn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C., Falls, T., Fan, G.,
Egan, A., Escottco, M., Eugene, C., Evans, C., Falls, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, M.,
Gebregeorgis, E., Habaland, W., Hamilton, C., Hamilton, C., Hamilton, K.,
Hernandez, R., Hines, S., Hullyk, S., Hume, J., Idlebird, D., Jackson, A.,
Hernandez, R., Hines, S., Hullyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jack, S., Hullyk, S., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Li, Z., Liu, J.,
Liu, J., Liu, J., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, J., Lousedo, R., Johnson, R.,
               Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reucer, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shataman, S., Shen, H.,
Shatery, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, J., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Miczyk, R., Wooden, H., Worley, K.,
Williams, G., Willson, R., Miczyk, R., Wooden, H., Worley, K.,
Willson, R., Mu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Dhou, J., Zhou, X., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
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HTG; HTGS_PHASE1; HTGS_
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muzny, D.Marie.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Consensus quality: 199255 bases at least Q40
Consensus quality: 203424 bases at least Q30
Consensus quality: 206379 bases at least Q20
Estimated insert size: 195822; sum-of-contigs estimation
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3: gap of unknown length
0: contig of 32587 bp in length
0: gap of unknown length
1: contig of 1413 bp in length
3: contig of 1413 bp in length
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                                               Rattus norvegicus clone CH230-112K14, ***, 7 unordered pieces.
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NAISM Entius norvegicus (Norway rat)

Rattus norvegicus (Norway rat)

Rattus norvegicus (Norway rat)

Rammalia (Eduaryota, Metazoa, Choradra, Craniata, Vertebrata, Buteleostomi, Mammalia (Eduaryota, Metazoa, Choradra, Craniata, Vertebrata, Buteleostomi, Mammalia (Eduaryota, Metazoa, Choradra, Carlota, Marine, Marine,
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Best Local Similarity: Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
  US-10-627-571-2 (1-188)
                                                                                                                                                                                             Pred. No.:
                                                                                                                                                                                                                          Alignment Scores:
                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                    misc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                              _feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4843
265127
265227
265730
2668730
266870
268870
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268970
270128
270128
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Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: CH230-112K14
Center clone name: Atlas 3.0;
Consensus quality: 224959 bases at least Q40
Consensus quality: 227786 bases at least Q30
Consensus quality: 227786 bases at least Q20
Consensus quality: 229294 bases at least Q20
Estimated insert size: 236137; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                 end_sequence:BH258362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (4198. .4940)
                                                                                                                                                                                                                                                                                                                                                                                          Site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                        note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="CH230-112K14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                    note="wgs_contig"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4842: contig of 4842 bp in length
,4942: gap of unknown length
265126: contig of 260184 bp in length
265226: gap of unknown length
266729: contig of 1503 bp in length
266829: gap of unknown length
268869: gap of unknown length
268869: gap of unknown length
26899: gap of unknown length
270127: contig of 1158 bp in length
27027: gap of unknown length
271518: contig of 1291 bp in length
271618: gap of unknown length
x AC129440 (1-273225)
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633.00
87.91%
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                                                                                                          Length:
Matches:
Conservative:
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                                             273225
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REFERENCE
AUTHORS
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ORGANISM
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AC118938/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                               Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaNocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., McCarthy, M., McEwan, P., McGarnan, K., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., Major, J., Marquis, N., Matthews, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Pollara, V., Pich, P., Pierre, N., Pich, P., Pierre, N., Pollara, V., Pich, P., Pierre, N., Pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP Mus musculus (house mouse)
Mus musculus
Oliver,J., Peterson,K., Phunkhang,P., Fierre,N., Furration, Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Butheria; Ro
1 (bases 1 to 164258)
Birren,B., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC118938 164258 bp
Mus musculus clone RP24-174015,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ហ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC118938.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnPro 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGlu 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAACCATGTCTTCAACCACTTCGCTGATGTGGAATTCCTTTCCACTCTACAGTCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 164258)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WORKING DRAFT SEQUENCE;
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NCE; 8 unordered
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REFERENCE TITLE JOURNAL

> Research, Submitted

AUTHORS

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Boguslavkiy, L. Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gadyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, L., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McGarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McGarthy, M., Meldrim, J., Weneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Rachupka, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tayarers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 24, 2003 this sequence version replaced gi:28261544. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Taing, T., Taing, T., Taing, T., Ye, W.J., Young, G., Taing, T., Taing, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                 as soon as in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 164258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name: L25165

Center clone name: 174 0 15

Center clone name: 174 0 15

Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 162666 bases at least 040

Consensus quality: 162865 bases at least 020

Consensus quality: 163183 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 164000; agarose-fp Insert size: 163558; sum-of-contigs Quality coverage: 11.0 in Q20 bases; Quality coverage: 11.0 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 Charles Street, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ., Zembek,L., Zimmer,A. and Zody,M.
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29707: contig of 29707 bp in length 29807: gap of 100 bp 32340: contig of 2533 bp in length 32440: gap of 100 bp 37689: contig of 5249 bp in length 37789: gap of 100 bp 104529: contig of 66740 bp in length 104629: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 SerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeu 44
                                                                                                                                                                                                                                                                                                 GAGGTTATAATTGTGGAGAAAACTCCGGAAGAAACTGAACCAGACTGCGATGACCATGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAsp 84
                                                                                                                                                  AGCTTCTACGAAGTAGAGTATACCTTTGATACGAATGTGCTCTCTAAGCTTCTGCATGAG
                                                                                                                                                                                                                                                                                                                                                                 GluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValVal 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsn 64
                                                                                                                                                                                                       SerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGlu 124
                                                                       CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAAAGTCACAGAAATACACACCCACAACAAGAAGGAGGCCCACAAGATCATGAAGGAT 87812
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vector_side:right"
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131778. .158793
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104630. .115026
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vector_side:left"
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'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_lib="RPCI-24 Male Mouse
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115126: gap of 100 bp
131677: contig of 16551 bp in length
131777: gap of 100 bp
158793: contig of 27016 bp in length
158893: gap of 100 bp
164258: contig of 5365 bp in length.
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626.00
86.26%
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Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BAC"
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LOCUS DEFINITION

VERSION KEYWORDS

ORGANISM

ACCESSION

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AUTHORS

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AUTHORS TITLE

Wu, X.,

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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ginde, S., Gord, S., Goyette, M., Gradham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Gradham, L., Grand-Pierre, N., Ginde, S., Gord, S., Goyette, M., Gradham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Marquis, N., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., Macdonald, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Norbu, C., Norman, C., H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Rilby, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Voa, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Direct Submission
2E 3 (bases 1 to 1955-8)

RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Frereira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C., MacConald, P., Major, J., Manning, J., Matches, G., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalla; buckler, 1 to 195574)

1 (bases 1 to 195574)

Birren, B., Nusbaum, C. and Lander, E.

Birren, B., Standar, C. and Lander, E.

Chromosome 9, clone RP23-321A19
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnPro 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAsp 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 195574)
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          No.:
                                                                                                                                                                                                                       160005 GTGTTTAGTTCCAAGAATCTCGCCCTTCAAGCCCAGAAGAAGATCCTGAGCAAGATAGCC 160064
                                                                                                     160065 AGCAAAACTGTGGCCAACATGCTGATTGATGACACCAGCAGTGAGATCTTTGATGAGCTG
                                         45
                                                                                                                                        25 SerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2004 this sequence version replaced gi:44886703.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vassiliev,H., Venkataraman,V.S., Viel,R., V
Wyman,D., Young,G., Zainoun,J., Zembek,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,XWyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
      TyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsn
                                                                                                                                                                                                                                                          ValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available be preserved.
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28331
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Center clone name: 321_A_19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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7979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP23-321A19"
/clone_lib="RPCI-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA
/db_xref="taxon:10090"
/chromosome="9"
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28230: contig
28330: contig
28330: contig
59488: contig
59588: gap of
100956: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195574
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195574: contig of 41211 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142783: gap of 
154263: contig
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142683: contig
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gap of 100 bp
contig of 20252 bp in length
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g of 2478 bp :
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Indels:
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of 39049 bp in length
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of 41368 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
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of 11480 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
of 31158 bp in length
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ORGANISM
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                                                                                        TITLE
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Strauberg, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Casvant, D.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevbhenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis MGC83729 protein, IMAGE:6639647), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetic and genomic tools for Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein, S.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg
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mRNA (cDNA clone MGC:83729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The NIH Xenopus
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                             Alignment
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                                                                                    151 TTTAGCTCAAAGAGCTTTGCTGTTCAAGCCCAGAAGAGTTCTCAGTAAGATGGCAACA
                                                                                                                                                                                                                                                                                                      Similarity:
26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Cgapbs r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 1777)
Klein, S. and Gerhard, D.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 158 Row: d Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
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Contact: XGC help desk
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20892-7510, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution
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                                                                                                                  PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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VENFRKKLNQTGMTAVSFFEEVEYTFDCMVLSGLLHECTLLHELVQRHIJTPKSHSRID
VENFRKKLNQTGMTAVSFFEEVEYTFDCMVLSGLLHECTLLHELVQRHIJTPKSHSRID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="LocusID:446389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="MGC83729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tissue_type="Oocytes"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:8355"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Xenopus laevis"/
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63.10%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _type="mRNA
                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
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Indels:
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                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.K.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Boutfard, G.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

PL 12479312
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                          Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 1813)
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                                                                                                                Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGACCATGGCCAACATGCTTATTGATGACACAAGCAGTGAAATATTTGATGAGCTCTTT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAspGlu 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAGGGTTTTTAATCATTTTGCTGATGTGGAATTCCTTACTGCCCTCTATAGCCCTTGAA 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgVal 145
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                                                                                                                                                                          (bases 1 to 1813)
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  LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer 105
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Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLML at: http://image.llnl. Series: IRAK Plate: 117 Row: e Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency OR analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicine, Stanford, CA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dickson,
/product="hypothetical protein MGC63960"
/protein id="AAH53167.1"
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VERFKKKMNQAAMTVVSFYEVEYTFDRGILSEILLECRDLHELVEHHLTMRSHGRID
HVFNHFADVDFLTELYGPSEDYRLNLRKICDGINKLLDEGTL"
                                                                                                                                                                                                                                                                                                            /note="synonym: MGC63960"
/db_xref="LocusID:393322"
178. .786
                                                                                                                                                                                                                                                                                /gene="zgc:63960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="Kidney, zebrafish"
/clone_Tib="NCI_CGAP_ZKid1"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="MGC:63960 IMAGE:6791907"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                         /gene="zgc:63960"
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US-10-627-571-2 (1-188) x BC053167 (1-1813)
                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
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IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                     ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
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                                                                                                                                                                         LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
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                                                            AAGGCCAGTCGAGAATACACCAAGAGCAAGAAGGAAGCCCCACAAGATCATCAAAGATGTC
                                                                                                                                                ATGGCCGTGGCGAACCTCCTAACAGACGACCAGCAGCGAGATTCTGGACGAACTCTAC
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58.89%
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RESULT 43
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                                                                                                                                                                                                                                                                                                                                               Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 134439 bases at least Q40
Consensus quality: 134480 bases at least Q30
Consensus quality: 134490 bases at least Q20
Insert size: 134497; sum-of-contigs
Insert size: 13631; 6.0% error; agarose-fp
Quality coverage: 10.02x in Q20 bases; sum-of-contigs Quality
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CR407586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (25-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 134497)
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Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: zC283G6
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                                                                                                                                                                                                                                                                                                                                     coverage: 9.90x in Q20 bases; agarose-fp
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                                                                                                                                                                                                                                                                       This sequence will be replaced
                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACCACGTTTTCAACCATTTCGCCGATGTGGATTTCCTGACCGAGCTGTACGGCCCATCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aug 26, 2004 this sequence version replaced gi:50871872
                                                                                                                                                                                                                               the finished sequence as soon as it is available and accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rerio clone CH211-283G6,
                                   clone_end:T7
          vector_side:right"
                                                                                                           /organism="Danio rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="HZ11-283G6"
                                                                                                                                                                                                               Location/Qualifiers
                                                 note="assembly_fragment:00151
                                                                                             clone_lib="CHORI-211"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
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                                                                       Submitted (08-OCT-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@ssanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 9, 2004 this sequence version replaced gi:52137684.
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 189797)

Mashreghi-Mohammadi, M.
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Zebrafish DNA sequence
Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                      Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                           Danio rerio
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                                       Center code:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAspGlu 185
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from clone
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CH211-12A1 in linkage group
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During sequence assembly data is compared from overlapping clones.

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US-10-627-571-2 (1-188) x BX927313 (1-189797)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                     167554 AAGGCCAGTCGAGAATACACCAAGAGCAAGAAGGAAGCCCACAAGATCATCAAAGATGTC 167495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167614 ATGGCCGTGGCGAACCTCCTAACAGACGACACCAGCGAGATTCTGGACGAACTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession mumbers given in the feature table with their source databases:

Em: _RMBL; Sw: _SWISSPROT; Tr. _TRBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where submitted
                                                                                                                                                                                                                                                                                                                                                                              66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lab, WashU). For further information see
http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-12A1
                                                                                                                                                                                     ATGGAGACAGTGGAGCGCTTCAAAAAGAAGATGAACCAGGCGGCCATGACAGTGGTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
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ArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgVal
                                                                TTTTATGAAGTGGAGTACACATTCGACCGAGGCATTCTTTCAGAGCTGCTGTTGGAATGT
                                                                                                                                                                                                                                         LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
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/clone="CH211-1070"
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/clone_lib="CHORI-211"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-dUL-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Mational Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. Cosmid R33729 overlaps BAC 48708 to the left from bases 1 to 8,574 and overlaps cosmid R26894 to the right from bases 26,845 to 32,360. Additional chr 19 map and sequence information are available at: http://www-bio.llnl.gov/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W., Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S., Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J., Danganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J., Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G., Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G., Krommiller, B., Areilano, A., Montgomery, M., Ow. D., Nolan, M., Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V. Sequence analysis of a 1 Mb region in 19p13.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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                                                                                                            /rpt_
                                                                                                                                                                                                                                                                                       /rpt_family="AluSx"
complement(354. .69
                                                                       complement (2197.
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                                                                                                                                                        /rpt_
1562.
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710. .787
                                                                                                                                                                                                                                                                                                                                                        carries chromosome 19 as its only human chromosome
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                                                                                                                                                                                                                rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                             chromosomes from human-hamster hybrid 5HL2-B, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell
rpt_family="GC_rich"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                clone
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                                     _family="AluSx"
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                                                                                                                                      y="AluJb"
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complement (5239) . 5545)
/rpt family="AluSx"
5741 . 5848
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complement (6054. .6181)

/rpt_family="FLAM_C"

complement (6188. .6262)

/rpt_family="MERSA"
                                                                                                                                                                                                                                                                                                                                   complement (13408..13671)
/rpt family="AluSq"
complement (13674..13880)
                                                                                                                                                                              complement(14560. .14854)
/rpt_family="AluSx"
complement(14865. .15172)
/rpt_family="AluJo"
                                                                                                                                                                                                                                                 complement (14175. .14555)
/rpt_family="L1MB7"
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/rpt_family="AluY"
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complement(11856..12145)
/rpt_family="AluSx"
                                                                                                         complement (16172. .16474)
/rpt_family="AluSq"
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complement(9773. .1
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7764. .7895
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Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                         /complement (24790. .25329)
/notes DBS similarity to overlapping ESTs:
/notes DBS similarity to overlapping ESTs:
(25329. .25201) AA477269 zu43c12.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone 740758 3'; (401. .273); 100% identity.~(25329. .25201) A477268 zu43c12.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 740758 5'; (221. .349); 100% identity.~(25329. .25201) A477268 zu43c12.rl Soares ovary tumor NbHOT Homo sapiens cDNA clone 740758 5'; (321. .349); (350. .570); 98% identity.~(24792. .25272) N32339 yw82g08.sl Homo sapiens cDNA clone 258782 3'. Score: 925 Identity: 476/480 (99%).~(25329. .25028) AA579149 nf28a04.sl NCI CGAP Prl Homo sapiens cDNA clone IMAGE: 918054; (134. .434); 99% identity.~(24790. .25061) AA477269 zu43c12.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone TA477659 zu43c12.sl Soares ovary tumor NbHOT Homo sapiens cDNA clone TA6786.
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23246, .2340*
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complement(21587. .21852)
                                                                                                                                                                                                             AA581955, AA467935, AI038745, AI041764, T24716"
complement(join(25250. .25329,27176. .27248,27914. .27995,
32121. .>32185))
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complement(21329. .21549)
/note="BLASTN similarity
score: 9.7e-83; database
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/rpt_family="FLAM_C"
complement(18725...18991)
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/rpt_family="AT_rich"
18551_ .18586
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22809. .22929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA sequence"
21389. .21554
                                                                                                     /evidence=not_experimental
/product="R33729_1"
/protein_id="AAC27824.1"
/db_xref="GI:3355455"
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22943. .23243
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                                                                                                                                                                                             note="Hypothetical partial human protein"
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593.00
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56.68%
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_quality: excellent, score: 92.000"
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Qy 182 MetLeuAspGluGluAsnIle 188 19652 ATGCTGGACGAGGCAGCCTC 19672	Qy 162 TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLys	Qy 142 HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu	Qy 122 LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer	Qy 102 ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu	Qy 82 AsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMet	Qy 62 IleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPhe ::: ::: Db 19292 CTCAAGAACCTGGTCAAGGTGGCCCTGAAGCTGGGACTGCTGCGTGGGACCAGCTG	Qy 42 AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys	Qy 22 LysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeu	Qy 2 AlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGly 21 ::::: ::: :::	Query Match: 61.64% Indels: DB: 9 Gaps: US-10-627-571-2 (1-188) x AC005339 (1-32360)
	InLysLeuCysAspGlyIleAsnLys 181 	erAspCysGluPheLeuAlaAlaLeu 161 :: :: CCGACTGCGACTTCCTGGCTGCGCTC 19591	leGlnArgHisLeuThrAlaLysSer 141 :: rGGGTCCCCACCTGACCGCCAAGTCC 19531	heAspArgAsnValLeuSerArgLeu 121 CGACCGGCGCGTGCTGGCCGCCGGG 19471	ysLysLysValHisGlnLeuAlaMet 101 :: GCCACCGGGCGCGCTGCCTGGCCATG 19411	lalleLeuTyrArgAsnAsnGlnPhe 81 	InAsnLysLysGluAlaGluLysLys 61 :::::: ::: GCAGCCGCAAGGAGGCCCAGAAGATG 19291	leAspAspThrSerSerGluValLeu 41 :: :GATGACACCAGCAGTGAGGTGCTG 19231	alGlnAlaGlnLysLysIleLeuGly 21 ::	

Search completed: July 28, 2005, 20:50:53 Job time: 4523 secs

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Title:
Perfect score:
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-MODEL-frame+ p2n.model -DEV=xlh
-Q-/GGR2_1/USPTO_Spool_h/US10627571/runat_27072005_154721_27515/app_query.fasta_1.327
-DB=Issued_patents_NA -QFMT=fastap_-SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=45
-MODE=LOCAL -QUTFMT=pto -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US10627571 @CGN 1 1 69 @runat 27072005 154721 27515 -MCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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Sequence 537, App
Sequence 14427, A
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Sequence 14434, Ap
Sequence 6176, Ap
Sequence 3950, Ap
Sequence 3008, Ap
Sequence 307, App
Sequence 39, Appl
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Sequence 1081, App Sequence 498, Appl Sequence 4175, Appl Sequence 417, Appl Sequence 17, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 19, Appl Sequence 11, Appl Sequence 17, Appl Sequenc
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: pt_FL_genes
SEQ ID NO 537
                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILING DATE: 2001-03-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6783969el Nucleic Acids
TITLE OF INVENTION: Polypeptides
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryl
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 948
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                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Zhang, Jie
Xue, Aidong J.
Zue, Aidong A.
I: Wang, Jian-Rui
T: Ma, Yunqing
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Yang, Yonghong
Wehrman, Tom
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Chen, Rui-hong
Wang, Zhiwei
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Zhang, Jie
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APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: Expressed Sequence Tags and Enc.
Patent No. 6783961
Patent No. 6783961
PILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14427
LENGTH: 340
TYPE: DNA
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GENERAL INFORMATION:
                  FEATURE:
NAME/KEY: misc_feature
TOTATION: 221
TOTATION: r=a
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NAME/KEY: misc_feature
LOCATION: 139
OTHER INFORMATION: w=a
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LOCATION: 208
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LOCATION: 170
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CGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
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NAME/KEY: misc feature LOCATION: 32
OTHER INFORMATION: y=c o US-09-513-999C-14434
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APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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SOFTWARE: PATENT.PM
SEQ ID NO 14434
LENGTH: 252
Sequence 6176, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
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LENGTH: 1347
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ORGANISM: Candida
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                                                               184 AspGluGluAsnIle 188
                                                                                                                                                                                               144 ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn
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                                 GACGATCAAACCGTA
                                                                                                                                ProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu
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CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILLING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILLING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILLING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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GTTTTTGAATATTTTTTG 1839
                                                                                                                           GCAAAACAAAAGAAACATGATTTGATAATAAATGATTTGAAT---
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                                                                                                                                                    ---LysLysLysValHisGlnLeuAlaMetThrValValSerPheHisGlnValAspTyr 111
                                                                                                                                                                                                                                                                                                                    AATTTGCGTTCTGAGCTAGGTGATGCTATGCATATGAAAAATGATCTTTTATCGAATCTA 1611
                             IleIleGlnArgHisLeu 137
                                                                                                                                                                                        TTGCAATTGAAATTGGATGAAATTAATGAAGATTATGAAAATCTTATGGAATTGACTCAA
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                                                                                       ThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGln
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RESULT 6
US-09-949-016-3908
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Best Local Similarity:
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 207012
SOFTWARE: FABESEQ for Windows Version 4.
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/99/949,016
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TYPE: DNA
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                                                                                                     LeuThrAlaLysSerHisGlyArg------ValAsnAsnValPheAspHisPhe
                                                                                                                                                           GAGGATGTGTTGGTCAGAGCCACCTGTATAGAAATGGTGACATCACTGGCATATACTCAT
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-----AspCysGluPheLeuAlaAlaLeuTyrAsnPro-----
                                                     ----CATGGGCGACAATATCTTGCTCAAGAAGGAGTAATTGACCAAATT 762
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US-09-976-594-907
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 907
LENGTH: 5923
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 907, Application US/09976594
Patent No. 6673549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 977975.1
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                        AACTTGAAG
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                                                                                                                                                                                                                                                                                           AlaLeu-----
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                                                            ThralaLys 140
                                                                                                                                  LeuLeuAsnGluCys-----ArgGluMetLeuHisGlnIleIleGlnArgHisLeu
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                                                                                              CTTAAGAAAAAATGTGGTGAAGACCAGGAGAAAATACACGCTCTCACATCTGAAAAACACT 265
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; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-39
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APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND
TITLE OF INVENTION: UREALYTICUM
PILE REFERENCE: UAB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
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SEQ ID NO 39
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Patent No. 6531583
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APPLICANT: Chen, E
APPLICANT: Glass,
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139 AlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 AlaGluLysLysIleLysAsnLeuIleLysThr----
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                                      ACTAATTTAAAACAAAATCTAAACAAGAATATCACTAATATTGTTAAT--
                                                                                                                                                  ThrValValSerPheHisGlnValAspTyrThr-----PheAspArgAsnValLeu 118
                                                                        SerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThr 138
                                                                                                                                                                                                                                                                                                       GluLeuAlaLeuMetGluLysPheLys-----
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SEQ ID NO 1
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TITLE OF INVENTION:
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CURRENT FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
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Best Local Similarity:
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CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: US 08/916,421
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
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                               NAME/KEY: misc feature
LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals
                                                                                 LOCATION: (981\overline{70})..(98120)
OTHER INFORMATION: n equals
FEATURE:
                                                                                                              NAME/KEY: misc_feature
LOCATION: (98120)..(98120)
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OTHER INFORMATION: n equals
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equal
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LOCATION: (28222)..(28)
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NAME/KEY: misc_feature
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NAME/KEY: misc_feature
LOCATION: (559167)...(559167)
OTHER INFORMATION: n equals
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LOCATION: (319226)..(319226)
OTHER_INFORMATION: n equals
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals
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LOCATION: (312837)..(312837)
OTHER_INFORMATION: n equals
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals
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LOCATION: (309398)..(309398)
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals
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LOCATION: (163385)...(163385)
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LOCATION: (98266)..(98266)
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LOCATION: (559241)..(559241)
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LOCATION: (234220)..(234220)
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LOCATION: (234187)...(234187)
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LOCATION: (191995)..(191995)
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LOCATION: (148948)..(148948)
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LOCATION: (103998)..(103998)
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OTHER INFORMATION: n equals a, t
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NAME/KEY: misc_feature
LOCATION: (1095846) ...(1095846)
OTHER INFORMATION: n equals a, t
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LOCATION: (741684)..(741684)
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LOCATION: (713652)...(713652)
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LOCATION: (674435)...(674435)
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LOCATION: (657081)..(657081)
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LOCATION: (622708)..(622708)
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                                       NAME/KEY: misc_feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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LOCATION: (871619)..(871619)
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LOCATION: (85539)..(85539)
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LOCATION: (779676)..(779676)
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LOCATION: (779455)...(779455)
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Sequence 8, Application US/09175684A

Patent No. 6593463

GENERAL INFORMATION:

APPLICANT: Chen, Li How

APPLICANT: Meade, Harry M.

TITLE OF INVENTION: NOVEL MODIFIED MSP-1 NUCLEIC ACID

TITLE OF INVENTION: SEQUENCES AND METHODS FOR INCREASING MRNA LEVELS AND PROT

TITLE OF INVENTION: EXPRESSION IN CELL SYSTEMS

FILE REFERENCE: 10275-133001

CURRENT APPLICATION NUMBER: US/09/175,684A

CURRENT ETLING DATE: 1998-10-20

PRIOR APPLICATION NUMBER: US 60/085,649

PRIOR APPLICATION NUMBER: US 60/062,592

PRIOR APPLICATION NUMBER: US 60/062,592

PRIOR FILING DATE: 1997-10-20

NUMBER: OF SEQ ID NOS: 19
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LOCATION: (1349473)..(1349473)
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN (
TITLE OF INVENTION: WITH HUMAN DISEASE, ME'
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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LENGTH: 1142
TYPE: DNA
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APPLICANT: VENTER, J.
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LOCATION: (1)...(1142)
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US-09-016-434-1081
Sequence 1081, Application US/09016434
Patent NO. 650038
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 975
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                      136
                                                                                                                                                                                                                                                                                                                                                                                                                                  96 ValHisGlnLeuAlaMetThrValValSerPheHisGlnValAspTyrThrPheAspArg 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76
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                                                                                                                                                                CysAspGlyIleAsnĻysMetĻeuAspGluGluAsn 187
                                                                                                                                                                                                   AAACCTTTGGCTTGTCTGCTGTTATCCCTAGAGAGTTTCTATCCTCCTGCTCATCAGCTA
                                                                                                                                                                                                                                GluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeu 175
                                                                                                                                                                                                                                                                                                   HisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCys 155
                                                                                                                                                                                                                                                                                                                                                          AsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArg 135
                                                                                                                                                                                                                                                                                                                                                                                                        CTACATGAACTTGTTATCAAAACCCTTGTCCAGCACAACCTTTTTAT-------
                                                                                                                                                                                                                                                                         CACGTC-----
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Janice Au-Young
Jeffrey J. Seilhamer
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Best Local Similarity:
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CORRESPONDENCE ADDRESS:
ADDRESSES: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No.:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               Match:
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STATE: CALIFORNIA
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                                                                                                                  GGCAAGAGTACGTTTATCAAGCAGATGAGAATCATCCATGGGTCAGGATACTCTGATGAA
                                                                                                                                                                                                                     GlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIle--------
                                                                               AspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrVal
                                                                                                                                               -----LysThrVallleLys---LeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGln
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Matches:
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Mismatches:
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-023-655-898
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US-09-023-655-898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cocks,
                                                                                                                                                                                                                                                                                TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 5.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION HEREWITH
CLASSIFICATION:
CLASSIFICATION:
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
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                                                                                                                                                                                                                                                                                                                                              NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
REFERENCE/DOCKET NUMBER:
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CITY: PALO ALTO
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Query Match:
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                                                                                   Percent Similarity:
                                                                                                                                                                          US-09-270-767-14175
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                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
SEQ ID NO 14175
LENGTH: 1865
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14175, Apparent No. 6703491
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                         ORGANISM: Drosophila melanogaster FEATURE:
                                                                                                                                                                                           OTHER INFORMATION:
                                                                                                                        20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           635 CCTGGAATCCAGGAATGCTATGATAGACGACGAGAATATC
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                                                                     Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLys-Le 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuThrAlaLysSerHisGlyArg---ValAsnAsnValPheAspHisPheSerAspCys 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHis 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATAAA------AGGGGCTTCACCAAGCTGGTGTATCAGAACATCTTCACGGCC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCAAGAGTACGTTTATCAAGCAGATGAGAATCATCCATGGGTCAGGATACTCTGATGAA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIle----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ThrSerSerGlu------ValLeuAspGluLeuTyrArgValThrArgGluTyrThr 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGCAGGCCATGATCAGAGCCATGGACACACTCAAGATCCCATACAAGTATGAGCACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LysThrValIleLys---LeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGln 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09270767
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x US-09-270-767-14175 (1-1865)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGCTCATGCACAATTAGTTCGAGAAGTT
                                      0.196
88.50
38.55%
22.91%
9.20%
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                                                                                                                                                                                         any nucleotide
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                                                  Conservative: Mismatches: Indels:
                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                    of Drosophila melanogaster
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Sequence 3485, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUMBER: US/09/710,279
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTMARE: PATENTIN Ver. 2.1
SEQ ID NO 3485
LENGTH: 3204
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                                                                                   Best Local Similarity:
Query Match:
DB:
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US-09-710-279-3485
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                                                     US-10-627-571-2 (1-188) x US-09-710-279-3485 (1-3204)
                                                                                                                                                      Pred. No.:
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                                                                                                                           Percent Similarity:
                                                                                                                                                                                                US-09-710-279-3485
                                                                                                                                                                                                        FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                 TYPE: DNA
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                       23 MetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAsp
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 TTGATGAGTAAAGAAGTATCGATAAGATATCTACAAGATAGAGATGGAGAA----
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                                                                                                                                                                                                           Description of Artificial Sequence: synthetic nucleic acid sequence
                                                                                              0.442
88.50
39.41%
22.66%
9.20%
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    ValAspTyrThrPheAspArgAsnValLeuSerArg

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Matches:
Conservative:
Mismatches:
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46
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59
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                                    Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-627-571-2 (1-188)
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                                                                                   Score:
                                                                                              Pred. No.:
                                                                                                           Alignment
                                                                                                                                                 FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
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US-09-710-279-4311/c
; Sequence 4311, Application
; Patent No. 6703492
                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: KIMMERLY, WILLIAM JOHN

APPLICANT: KIMMERLY, WILLIAM JOHN

ITITE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

FILE REFERENCE: PU3480US

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258

PRIOR FILING DATE: 1999-11-09

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PACENTIN Ver. 2.1

SEQ ID NO 4311

LENGTH: 3627

TYPE: DNA
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 IleGlnArgHisLeuThrAlaLysSerHisGly-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 ValHisGlnLeuAlaMetThrValValSerPheHisGlnValAspTyrThrPheAspArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAGCAAATGGAGACGGTATAGCTGAAACAAAACAAGCCAGAGTATCAATAGATGGTACC
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Percent Similarity:
Best Local Similarity:
                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: nucleic acid sequence US-09-710-279-4029
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                                                                       Alignment Scores: Pred. No.:
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PATENT NO. 6703492
GENERRAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 1090-11-09
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
PRIOR PRIOR SEQ ID NOS: 4472
                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4029
LENGTH: 3760
                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                 TYPE: DNA
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TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND
THEIR OF INVENTION: ATHEROSCLEROSIS
FILE REPERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT APPLICATION NUMBER: US/09/517,849
FRIOR APPLICATION NUMBER: US 09/517,849
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
PRIOR FILING DATE: 1996-11-27
PRIOR FILING DATE: 1997-06-03
NUMBER: OF SEQ ID NOS: 53
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DB:
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 46, Approx 8632923
                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                           APPLICANT: Law, Sin APPLICANT: Arjona,
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lees, Ann M. APPLICANT: Lees, Rober
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAGCAAATGGAGACGGTATAGCTGAAACAAAACAAĞCCAGAGTATCAATAGATĞĞTACC
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                                                                                                                                                                                                                                                                                                                                Law, Simon W.
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US-09-750-590A-3
; Sequence 3, Application US/09750590A
; Patent No. 6780987
; GENERAL INFORMATION:
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US-09-616-289-46
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SEQ ID NO 46
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                 CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGATGGAACAGCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCT
                                                                                                                                                  AAAAGCAGCGAGGTATTCACCACATTCAAGCAGGAGATGGAAAAGATGACTAAGAAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                AspTyrThrPhe------AspArgAsnValLeuSerArgLeuLeuAsnGlu 124
                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAG------GAGCATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSerPheHisGlnVal 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaileLeuTyr-----ArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeuMet
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                                                                                                                                                                                                                                                                                                 ValAsnAsnValPheAspHisPheSerAspCysGluPheLeu---------
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                                                                                                                                                                                                            CTGAAGCAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACTTTTCC
                                                                                                                                                                                                                               -----AlaAlaLeuTyrAsnPro-------
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US-08-979-608A-17; Sequence 17, Application; Patent No. 6355451
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PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: 09/733,818
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 25
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APPLICANT: Welch, Alice
TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL
TITLE OF INVENTION: ABNORMAL CELL MIGRATION
FILE REFERENCE: TUI-001CP
CURRENT APPLICATION UNMBER: US/09/750,590A
CURRENT FILING DATE: 2000-12-28
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 IleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 ArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIle-----LysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 AlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyrArgValThr 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 LysasnLeualaValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIle
GAATTTGTGAAAATAAAAGATGAGAACGAAATA
                                                                                                                                                                                                                                                          HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu 161
                                                                                                                                                                                                                                                                                                                                                              LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                    AAATGTGGTGAA------GACCAAGAGAAAATATATTCACTC
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                                             -----LysMetLeuAspGluGluAsnIle 188
                                                                                                   TTGGATAAAACCAATAGAGAATTAGTAGATGTGAAGAAGTAGTGTGAAGATATAAATCAA 2634
                                                                                                                                                 TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn--- 180
                                                                                                                                                                                                          CATGAAGAGATTAAAACTGCC-
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/031,930
FILING DATE: 27-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-00200
TELEPHONE: 617/542-5070
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/979,608A FILING DATE: 26-No. 6355451-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lees,
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     753
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                                                                                                                                                                                                                                                             14 GlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIleAlaThrThr-----
                                                                                                            GluLeuTyrArgValThrArg------GluTyrThrGlnAsnLysLysGluAla
                                                                                                                                                                                                                             CAGAAGCAGATGAAGCTCCTACAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCAC
 GAGGAGAAGCGCAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTG
                                     GluLysLysIleLysAsnLeuIleLys--
                                                                                                                                                  CTGCGCGGTGAGCACAGCAAGGCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGT
                                                                                                                                                                                         LeuIleAspAspThrSerSerGluValLeu------
                                                                         GAGCTGCAGCGGCACAACCGCTCCCTCAAGGAAGAAGGTGTGCAGCGGGCCCCGGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/048,547 FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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Robert S.
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Matches:
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US-09-517-849-17
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Patent No. 6605588
GENERAL INFORMATION:
               NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                              APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/979,608
FILING DATE: 26-NOV-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arjona, Anibal A.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USES
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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                                                                                            10797-003001
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IN DIAGNOSING AND

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US-09-616-289-17
; Sequence 17, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                 1221 AAGAAGCTGGAGAAAGAA
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                                                                                                                                                                                                                                               CTGAAAGAGGCAGTAGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCAC
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                                                                                                                                                                                                                                                                                                                             CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4697 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                         CTGAAGCAACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCC
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Matches:
Conservative:
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: Law, Simon W.
TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING TITLE OF INVENTION: ATHEROSCLEROSIS
FILE OF INVENTION: ATHEROSCLEROSIS
FILE OF INVENTION: ATHEROSCLEROSIS
FULL REFERENCE: 10797-004001
CURRENT APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 06/979,608
PRIOR APPLICATION NUMBER: US 60/979,608
PRIOR APPLICATION NUMBER: US 60/931,930
PRIOR FILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1996-11-27
PRIOR PILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FASTSEQ for Windows Version 4.0
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; NAME/KEY: CDS
; LOCATION: (3).
US-09-616-289-17
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Best Local Similarity:
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TYPE: DNA
ORGANISM: Homo sapiens
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145 ValAsnAsnValPheAspHisPheSerAspCysGluPheLeu-----
                                                                               984 GCCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAAGAAGGATTTT---CTC 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 73 AlaIleLeuTyr-----ArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeuMet 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 LeuIleAspAspThrSerSerGluValLeu------Asp
                                                                                                                                                                                                                                                                                          GAGAGGCTCAAGAAGCTGATTGAGCAGTATGAGCTGCGCGAG--
                                                                                                                                                                                                                                                                                                                                           GluLysPheLysLysValHisGlnLeuAlaMetThrValValSerPheHisGlnVal
                                                                                                                                CysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArg
                                                                                                                                                                                     GACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCAG
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Percent Similarity:
Best Local Similarity:
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SOFTWARE: FastSEQ for
SEQ ID NO 1
LENGTH: 4730
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APPLICANT: Welch, Alice
TITLE OF INVENTION: BETA-CAP73 CONTROL OF NORMAL
TITLE OF INVENTION: ABNORMAL CELL MIGRATION
FILE REFERENCE: TUI-001CP
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LOCATION: (39)
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ORGANISM: Bos taurus
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                   ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
                                                                                                                                                AGTAAAAATGTCAGCCGCCTGGAAACTGTGTTCATACCTCCCGAGAGACACGAAAAAGAA
                                                                                                                                                                                        IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                 CACAAATATACAGAAAAGAAGTTGGAAAATGGAAAGTTGCTTATGGAAAATGCCAGTTTA
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                                                                 ATGATGGCTCTGAAATCCAATATCACTGAACTTAAGAAGCAGCTGTCTGAACTTAATAAA 2836
                                                                                                                                                                                                                                                                    ArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIle-----LysAsnLeu
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Best Local Similarity:
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; NAME/KEY: misc feat
; OTHER INFORMATION:
US-09-976-594-940
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Patent No. 6673549
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ORGANISM: Homo sapiens
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                                                                                                                            1311 GATTTCCTGAAAGCTCAGCAAAAATACACCAACATTGTTAAAGAAATGAAAGCAAAGGAT 1370
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104 ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn 123
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                                                                                                                                                                  64 AsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGln
                                                                                                                                                                                                                                          45 TyrArgValThrArgGluTyrThrGlnAsnLys---LysGluAlaGluLysLysIleLys
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                                           CTTGAAATCAGGATACACAAGAAGAAAAAATGTGAAATTTATCGGAGACTGAGAGAGTTT 1430
                                                                                                                                                                                                           GTAGTCAACCTTCTCCGCATGACTCAAATCAAAATTGAAGAAAGGAACAAAAGTCCAAG
                                                                                 AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal
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Qy 4 AspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMet 23	RESULT 26 US-09-336-447A-2 ISEQUENCE 2, Application US/09336447A Patent No. 6310190 GENERAL INFORMATION: APPLICANT: HANSEN, ERIC J. APPLICANT: COPE, LESLIE D. APPLICANT: COPE, LESLIE D. APPLICANT: FISKE, MICHAEL J. APPLICANT: FISKE, MICHAEL J. APPLICANT: FREDENBURG, ROSS A. ITITLE OF INVERTION: USPA1 AND USPA2 ANTIGENS OF MORAXELIA CATARRHALIS FILE REFRENCE: AMCY:024 CURRENT PILLING DATE: 1999-06-21 UNUMBER OF SEQ ID NOS: 98 SOFTWARE: PATENTIN VEY: 2.1 SEQ ID NO 2 LENGTH: 3349 TYPE: DNA ORGANISM: Moraxella catarrhalis US-09-336-447A-2 Alignment Scores: Pred. No.: 87.50 Best Local Similarity: 40.364 CORSETVATIVE: 40.364 CORSETALE: 66 Ouery Match: 3 US-09-371-2 (1-188) x US-09-336-447A-2 (1-3349) US-10-627-571-2 (1-188) x US-09-336-447A-2 (1-3349)	Qy 182MetLeuAspGluGluAsnIle 188 ::::: :::	171 HisLeuGlnLysLeu	Qy 138ThralaLysSerHisGlyArgValAsnAsnValPheAsp 150	Db 1431 GCTAAACTGTATGACACCATTCGAAATGAAACAAATTTGTTAACTTACTCCAC 1487 Qy 124 GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeu
Alignment Scores: Alignment Scores: Bred. No.: 87.50 Matches: 47 Score: 87.50 Matches: 47 Percent Similarity: 40.36% Conservative: 43 Best Local Similarity: 9.10% Indels: 67 Query Match: 9.10% 4 Gaps: US-10-627-571-2 (1-188) x US-09-952-267B-2 (1-3349) Qy 4 AspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMet 23	Qy 165 PheGlyAsnPheLysDroHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu 183 Db 1827	Qy 151HisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnPro 164	132 IleIleGlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAsp	Qy 106 PheHis	Db 1503 GATGATGTTGCTGACAACCAAGATGACATAAAAAAAAAA

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RESULT 28
US-08-979-608A-14
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GENERAL INFORMATION:
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION NUMBER: US/08/979,608A
FILING DATE: 26-No. 6355451-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1827
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COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATAAGGAGGTGAAAGAGCTTGATAAGGAGGTGGGTGTATTAAGCCGAGACATTGGTTCA 1622
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                 APPLICATION NUMBER: US 60/048,547 FILING DATE: 03-JUN-1997
                                                                                                                                                                                                                      ZIP: 02110-2804
                                                                                                                                                                                                                                                                          CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheGlyAsnPheLysProHisLeuGlnLys---LeuCysAspGlyIleAsnLysMetLeu 183
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APPLICATION NUMBER: US 60/031,930
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Law, Simon W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert S.
                                                                                                                                                                                                                                                                                                                                                                       TREATING ATHEROSCLEROSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; SEQUENCE DESCRIPTION: US-08-979-608A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
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1309
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                     139 AlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                            961
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AAGATGACAAAGAAGATCAAGAAGCTGGAGAAAGAG 1344
                                  LysLeuCysAspGlyIleAsnLysMetLeuAspGlu 185
                                                                       TTCCAGAACACTCTTTCCAAAAGCAGCGAGGTGTTCACCACATTCAAACAGGAAATGGAA 1308
                                                                                                                                            AAGCAACAGGAGACCCACCTGAAGCAGCAGCTTGCCCTATACACAGAGAAGTTTGAGGAG
                                                                                                                                                                                                                    GAGAAGGACTTT----CTCCTGAAGGAGGCCGTGGAGTCCCAGAGGATGTGCGAGCTGATG
                                                                                                                                                                                                                                                                                           GACGCCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAGGCAGAGGAGCGGCACCAGCGG
                                                                                                                                                                                                                                                                                                                              SerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThr 138
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAACATGGAGCTGGCCGAGCGGCTCAAGAAGCTGATTGAGCAGTACGAGCTGCGAGAA 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIleLys------
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REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                   ----GAGCACATCGACAAAGTCTTCAAACACAAGGATCTGCAGCAGCAGCTGGTG 107
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36.79%
19.81%
9.10%
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                                                                                                                                                                               -----AlaAlaLeuTyrAsnPro-----
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Conservative:
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                                                                                                        PheGlyAsnPheLysProHisLeuGln
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US-09-517-849-14
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                                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                              Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: 10797-003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEPAN: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/517,849
FILING DATE: 02-Mar-2000
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/979,608 FILING DATE: 26-NOV-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                  781
                                                                                                                                        721
                                  53
                                                                                                 33 IleAspAspThrSerSerGluValLeuAspGluLeuTyrArgValThrArgGluTyrThr 52
                                                                                                                                                                     13 ValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIleAlaThrThrLeu 32
                CAGCGAGCCCGAGAGGAGGAGGAGGAGGAGGGAGGTGACGTCACACTTCCAGATGACG
                                                                  GTGCAGGAGAAGGACCACCTGCGTGGCGAGCACAGCAAGGCCATCCTGGCCCGCAGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence LOCATION: 61...1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4722 base pairs
TYPE: nucleic acid
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ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arjona, Anibal A.
INVENTION: NOVEL LOW DENSITY LIPOPROTEIN
BINDING PROTEINS AND THEIR USES IN DIAGNOSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Law, Simon W.
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19.81%
9.10%
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Matches:
Conservative:
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Indels:
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APPLICANT: Lees, Ann M.
APPLICANT: Lees, Robert S.
APPLICANT: Lees, Robert S.
APPLICANT: Law, Simon W.
APPLICANT: AIM, SIMON W.
APPLICATION NUMBER: US/09/616,289
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 09/517,849
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: US 08/979,608
PRIOR FILING DATE: 1996-11-27
PRIOR APPLICATION NUMBER: US 60/031,930
PRIOR APPLICATION NUMBER: US 60/048,547
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                                          Percent Similarity:
Best Local Similarity:
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                       Query Match:
                                                                                           Score:
                                                                                                                                   Alignment Scores:
                                                                                                                                                                                    US-09-616-289-14
                                                                                                                                                                                                                                                                                                                   SEQ ID NO 14
LENGTH: 4722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1997-06-03
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ
                                                                                                                                                                                                     ORGANISM: Oryctolagus FEATURE: NAME/KEY: CDS LOCATION: (61)...(1731
                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 GAGAAGGACTTT----CTCCTGAAGGAGGCCGTGGAGTCCCAGAGGATGTGCGAGCTGATG 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1072 GACGCCAAGCTCCAGCAGGCCCAGGAGATGCTGAAGGAGGCAGAGGAGCGGCACCAGCGG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 LysLeuCysAspGlyIleAsnLysMetLeuAspGlu 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeu 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 SerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThr 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 AspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrVal 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 ---ThrValIleLysLeuAlaIleLeuTyr-----ArgAsnAsnGlnPheAsnGln
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  1.07
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FILE REFERENCE: 1015
CURRENT APPLICATION NUMBER: US/09/541,782
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5
SEQ ID NO 5
LENGTH: 4223
TYPE: DNA
ORGANISM: S. pombe
US-09-541-782-5
      Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 31
US-09-541-782-5
                                                                                          Pred. No.:
                                                                                                          Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09541782
Patent No. 6284480
GENERAL INFORMATION:
APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysLeuCysAspGlyIleAsnLysMetLeuAspGlu 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValSerPheHisGlnValAspTyrThrPhe------AspArgAsnValLeu 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLysSerIleAlaThrThrLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----GAGCACATCGACAAAGTCTTCAAACACAAGGATCTGCAGCAGCAGCTGGTG 107
      1.05
87.00
41.71%
21.11%
9.04%
                      Length:
Matches:
Conservative:
Mismatches:
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    4223
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                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 32
US-09-723-820-5
    Query Match:
DB:
                                                                                      Score:
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                                                                                                                                                                                                                                                            SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/723,820
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 09/541,782
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                     TYPE: DNA
ORGANISM: S.pombe
                                                                                                                                                                                                                                     LENGTH: 4223
                                                                                                          No.:
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    Query Match:
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                                           Percent Similarity:
                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 5, Application US/10270085
Patent No. 6627408
                                                                                                                                                                                                                                 SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Nislow, Corey
APPLICANT: Sakowicz, Roman
APPLICANT: Beraud, Christophe
TITLE OF INVENTION: Antifungal Assay
FILE REFERENCE: 1015
                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/270,085
CURRENT FILING DATE: 2002-10-11
                                                                                                                                                                                      LENGTH: 42
TYPE: DNA
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                                                                                    No.:
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                                                                                                     Pred. No.:
                                                                                                                       Alignment Scores:
                                                                                                                                                                  US-09-248-796A-4746
                                                                                                                                                                                                     SEQ ID NO 4746
LENGTH: 2469
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4746, Application Patent No. 6747137 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Keith Weinstock et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
                                                                                                                                                                                        ORGANISM: Candida
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3253

73 693

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Query Match:
DB:
                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                            NAME/KEY: unsure; LOCATION: (3),(29),
OTHER INFORMATION:
US-09-248-796A-5857
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                                                                                                                          Alignment Scores:
                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 5857
LENGTH: 1299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5857, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR PILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -09-248-796A-5857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08462949
Patent No. 5606022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
       NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1B024-US1
TELECOMMUNICATION INFORMATION:
                                                                     ATTORNEY/AGENT INFORMATION: NAME: Robinson, Joseph R
                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE:
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212-527-7700
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Component Signal Transducing Regulatory
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TELEFAX:

201-753-6237

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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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HYPOTHETICAL:
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                                                                                                                         1171 CTTGAACTCGTGTGATATTGTTGATAAAGTCATTCTTCATTTC----TGTCAGCTT 1118
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                                                              CTTCTGGCG 1109
                                                                                             LeuAlaAla 160
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GENERAL INFORMATION:
APPLICANT: Rasmussen, Beth Ann
TITLE OF INVENTION: Cloning and
TITLE OF INVENTION: Component &
TITLE OF INVENTION: Bacteroidee
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1i
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LENGTH: 2651 base pairs
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APPLICATION NUMBER: US/08/023,764B
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ADDRESSEE: American Cyanamid Company
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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(201)831-3305
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Component Signal Transducing Regulatory
Bacteroides Fragilis
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Matches:
Conservative:
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-MetThrValValSerPheHis :::||||:::::::|||||||
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US-10-627-571-2 (1-188) x US-09-134-000C-1489 (1-618)
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Enterococcus faecalis US-09-134-000C-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACITITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
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US-09-134-000C-1489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                      184 GCACCTTCCATGGAAGAAATATCAAAGAAATTAAAAAGGCAGTCAAACGCATT-----
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                                                        LysLysGluAlaGluLysLysIleLysAsnLeuIleLysThrValIleLysLeuAlaIle
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                                                                                             TATGAATTTTCAGGAGAAAAATCTGGTATTTCTCTGAAAAAGTGATTGAGACGCAAGCG 183
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PCT-US94-01101-1
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APPLICANT:
                                                                                                                                                                                                                                                                      TELEPHONE: 617/720-3500
TELEPAX: 617/720-2441
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/
FILING DATE: FILED HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/005
FILING DATE: 15-JAN-1993
ATTORNEY AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B081
                                                                         ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: HOM
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
COERTIAL SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
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LENGTH: 1854 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: WOLF, GRE
                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
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Query DB:

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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US-09-949-016-5562
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        CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASICEQ for Windows Version 4.0
SEQ ID NO 5562
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                                                                                                                                                                                                                                                                                                     Sequence 5562, Application US/09949016 Patent No. 6812339 GENERAL INFORMATION:
                                                                                                                                                                                                                                       APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                           FILE REFERENCE: CL001307
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GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-00-09

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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TYPE: DNA
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APPLICANT: Lynn Douc
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LENGTH: 103
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674
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                             TYPE: DNA ORGANISM: Homo sapien
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Sequence 84, Application US/09404879A

Patent No. 6468546

GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46202
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
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Matches:
Conservative:
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Indels:
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THE THERAPY AND

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GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOI
TITLE OF INVENTION: OVARIAN CANCER
FILE REFERENCE: 210121.462C1
CURRENT APPLICATION NUMBER: US/09/338,933
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 312
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
LENGTH: 571
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Patent No. 6488931
                                                                                         TYPE: DNA
ORGANISM: Homo
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                                                                                                                                                   APPLICANT: Mitcham, Jennifer L.
APPLICANT: Frudakis, Tony N.
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: OF OVARIAN CANCER FILE REFERENCE: 210121.463
CURRENT APPLICATION NUMBER: US/09/215,681A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 310
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 84
LENGTH: 571
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DB:
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Best Local Similarity:
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                                                                                                            US-09-215-681-84
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                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 84, Application US/09215681A Patent No. 6528253
                                                                                                                           ORGANISM: Homo sapien
                                                                                                                                               TYPE: DNA
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Gaps: 1-2 (1-188) x US-09-215-681-84 (1-571) 7 AsmSerLysAssileuAlaValiGinAlaGinLysLysIlleLeuGlyLysMetValSerLys 8 ACAAGAAACACAAGAAGTTCAGCAACTTCAGGAAAACTTGAGACAGTACTGTAGCCAG 7 SerIleAlaThrThrLeuIleAspAspThrSerSerGiuValLeuAsp 8 CTTGCAGCCTTTACTAAGAGCATGTCTCCCTCCAGGATGATCTGTGACAGGTGATAGATGT 8 CILLeuTyrArgValThrArgGiuTyrThrGinAsmLysLysGiuAlaGlaAgaATTGAAGAGAGAGTGATGATGAAGAGAAACTTGAACGAGAGTGATGATAGAAGAAGAAGAATTTACTGAAGCAAAGAAGAAGAAGAATTTACTGAAGCAAAGAAAATTGAAAGAATTTACTGAAGCAAAGAAAATTGAAAGAAA	Search o	B 8	B &	δ δ g	3 8 8 8	D Q	₽ Q	유 성	B &	Qy dg	Query Match: DB: US-10-627-57
8.78% Indels: 33 4 Gaps: 8 4 (1-571) LysAssnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSerLys	completed: Ju : 1080 secs					81 PheAsr					atch: 27-571-2 (1-1
Indels: 33 Gaps: 8 **Il5-681-84 (1-571) **alGlnAlaGlnLysLysIleLeuGlyLysMetValSerLys 2	ily 28, 2005,	GlyIleAsnLysM ::: TCTTTAGAAAAAT	LeuAlaAlaLeuT TAGCTAAGTTGG	ThralaLysSerH	iLeuAlaMetThrv !AAGGCCCAGACAG iSerArgLeuLeuA	IGlnAspGluLeuA ::: !ATGGAAGAATTAA	ELYSASnLeuIleL CAAAGAAGATAATT	:TyrArgValThrA ::: PAAGAAATGGGAGA	AlaThrThr GCCTTTACTAAGA	CLysAsnLeuAlaV ::: AAAGACAAGGAAG	8.78% 4 (188) x US-09-2
33 8 2LysIleLeuGlyLysMetValSerLys 2 33 34 35 36 371) AspAspThrSerSerGluValLeuAsp 4 AspAspThrSerSerGracTGTGACCCAG AspAspThrSerSerGluValLeuAsp 4 34 35 CAGGATGATCGTGACAGGGTGATAGAT 36 36 37 38 38 38 38 38 38 38 38 38 38 38 38 38	19:39:58	etLeuAspGlu 18! :::::: GTAAGGAACAA 2	YrAsnProPheGly; ;AATCAGAACTTAAG; fetLeuAspGlu 18;	ISDGJUCYSARGGJU	alValSerPheHis	AlaLeu ;;; AAGATTAACATTTCC	ysThrVallleLys ::: ::: GCAGTGTTCTAAAG	.rgGluTyrThrGln :::::::: .GGAAGTTTAGTGAT	GCATGTCTTCCCTC	alGlnAlaGlnLys rrcagcaactrcag	Indels: Gaps: (15-681-84 (1-5
ysMetValSerLys 2		и	AsnPheLysProH ::: AGTCTCAAAGACC	AsnValPheAspH	GlnValAspTyrT	MetGluLysP ::: AGGCTTGAACATG	LeuAlaIleLeuT: ::: GATCAACTT	AsnLysL	AspAspThrSerS	LysIleLeuGlyL: ::: GAAAACTTGGACA	
			isLeuGlnLysLev AGTTGACTGATTTA	IAGARGAGACACGC isPheSerAspCys 	hrPheAspArgAsr AAC leIleGlnArg	heLysLysLysVal ::: aCAAGCAGATTTGC	yrArgAsnAsnGlr AGACAGATGTCC	ysGluAlaGluLys AAGAAGAAGAAATT	erGluValLeuAsp ::: aCAGGGTGATAGAI	y8MetValSerLy8 ::::: GTACTGTGACCCAC	
			1 175	8 155	1 116 1 173 1 135	96	1 80	326	386	1 26 1 446	

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Command line parameters:

-MODEL-frame+ D2n.model -DEV-xlh
-Q-[cgn2_1/USPT0_gpo2_l h/US10627571/runat_27072005_154719_27497/app_query.fasta_1.327
-Q-[cgn2_1/USPT0_gpo2_l h/US10627571/runat_27072005_154719_27497/app_query.fasta_1.327
-DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DCALIGN=200 -THR_SCONE=pct -THR_MAX=100 -THR_MN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM-ext -HEAPSIZE=50 -MINLEN=0 -MAXLEN=200000000
-USER=US10627571 @CGN 1 1_470 @runat_27072005 154719 27497 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSDELOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Aax56021 Merozoite
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Abx15269 P. falcip
Adm86686 Plasmodiu
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Ab124777 Drosophil
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Ab119373 Breast ca
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Abg92061 Human pol
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Adm39127 Cancer/an
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Acm39836 Tumour-as
Adl13178 Human mdd
Adf77343 Lactic ac
Aax99539 Nucleic a
Continuation (3 of
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Aca22957 Prokaryot
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Acn92808 Breast ca
Aah41227 Pyrococcu
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Aax20250 Borrelia
Aah03594 Human cDN
Aca47387 Prokaryot
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; T lymphocyte activation; T-cell; A-raf-1; TCPTP/PTPN2; asthma; immunosuppressive; antiasthmatic; antiallergic; antiinflammatory; lymphocyte activation; lymphocyte migration; cytokine production; cell surface marker expression; antibody production; apoptosis; allergy; antibody proliferation; antibody differentiation; hypersensitivity; antibody proliferation; antibody differentiation; hypersensitivity; graft versus host disease; inflammation; gene; ss; TNF-induced protein;
                                                                                                                  Identifying a compound that modulates T lymphocyte activation, useful for monitoring changes in cell surface marker expression, comprises contacting a T cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound.
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                       LysMetLeuAspGluGluAsnIle
                                                                                                                                   LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
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immunizing )
                                                                                                                                                                                                                                                                           The invention relates to an anti-apoptopic gene SSC-S2 and encoded protein. The gene is a positive mediator of tumour growth and metastasis in certain cancer types. The SSC-S2 protein can be expressed by standard recombinant methodology. The SSC-S2 polypeptide is useful as a target for identifying compounds that modulate cancer progression by inhibiting apoptosis, as a target for detecting cancers where this polypeptide is overexpressed, e.g. renal and overian cancers, and leukemia. The antibody and antisense oligonucleotide can be used to treat cancer and to inhibit cancer cell proliferation and/or metastasis. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  New SCC-S2 polypeptides and nucleic acids encoding them, useful as target for identifying compounds that modulate cancer progression inhibiting apoptossis, as a target for detecting cancers, or for immunizing animals.
                                                                                                                                                                                                                                                Sequence 1915
                                                                                                                                                                                                                                                                                                                                                                                               Claim
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CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
                                            GGTAAAATGGTGTCCAAATCCATCGCCACCATTAATAGACGACACAAGTAGTGAGGTG
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                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 ful length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                              27-AUG-1999; 99JP-00300253
11-JAN-2000; 2000JP-00118776
02-MAY-2000; 2000JP-00183767
09-JUN-2000; 2000JP-00241899
                                                                                                                                      WPI; 2001-318749/34.
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27-AUG-1999;
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, Sugiyama
                                                                                                                                                                                                                                                                                                                                                                 primer;
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                                                                                                                                                                                                                                                                                                                                                                                       sequence SEQ ID NO:12751
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                                                                                                                                                                                                                                                                                                                                                                  detection;
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                                                                                                                                                        Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
                                                                                                                                                                                                                                                                                                                                                                diagnosis; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВP
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A, Nagai
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Otsuki
                                                                                                                                                          Yamamoto T;
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The present invention describes primer sets for synthesising 56 length cDNAs defined in the specification. Where a primer set complementary to an oligo-dT primer and an oligonucleotide complementary to complementary to a polynucleotide which comprises one of

sequences defined in the specification, where

one of

Claim

8

SEQ ID

NO 12751;

2537pp +

Sequence Listing;

English

5602 full-

comprises:

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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end cCC sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence's end sequence is selected from those defined in the comprises at least 15 nucleotides and the combination of CC specification. The primer sets can be used in antisense therapy and in CC gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAH13633 to AAH19742 represent human cDNA sequences; AAB92446 to AAB95893 CC represent human amino acid sequences; and AAH13632 represent coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention
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                          LysMetLeuAspGluGluAsnIle 188
                                                                                                             LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                                                                                                                     SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                                                                                                                                                                                 LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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  AAAATGTTGGATGAAGAGAACATA
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AAH14793 ID AAH1

AAH14793 standard; cDNA; 1729

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US-10-627-571-2 (1-188) x AAH14793 (1-1729)

MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu

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Percent Similarity:
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                                                                                                                                                                                                                                                                              CC (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 cmucleotide sequences defined in the specification, where the coligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end complementary to a polynucleotide comprising a sequence complementary to a coligonucleotide which comprises a 3'-end sequence, where the coligonucleotide which comprises a 1'-end sequence, where the coligonucleotide comprises a 1'-end sequence, where the coligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in the comparison of the full-length cDNAs. The primers are useful for synthesising polynucleotides, carticularly full-length cDNAs. The primers are also useful for the comparison of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH30316 to AAH3328 and coligonucleotides, all of which are used in the exemplification of the coligonucleotides, all of which are used in the exemplification of the
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes primer sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUL-2000; 2000EP-00116126
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                                                        Similarity:
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, Sugiyama
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; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
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T, Wakamatsu
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ı A, Nagai K
                             Length:
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ARBSULT 5
ADR14214
ADR14214
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                                                                                                                                                                                                                                                                   antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic; immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; N-kappas regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;
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C gastrointestinal-Gen, antiasthmatic, antiarreriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or cuseful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an cimmune disorder, an inflammatory disorder, and inflammatory disorders, hyper-light syndromes, hyperidisory, viral inflammatory, hyper-light syndromes, hyperidisory, viral inflammatory, viral replication, host cell continued disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper companital conditions, birth defects, necrotic lesions, wounds, corgan transplant rejection, conditions related to organ transplant conditions, borth defects, necrotic lesions, wounds, corgan transplant rejection, conditions related to organ transplant corgan transplant sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the corgan transplant association with the NF-kappaB pathway of the corgan transplant and cordant sequence does not appear in the specification but was obtained by the indexer from Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention be useful for the production of compounds with an antiinflammatory,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
Sequence 1814 BP;
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12-MAY-2003; 2003US-0469757P
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Best Local Similari
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LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autolamune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; hodgkin's lymphoma; haematopoletic tumour; hyperIgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response; viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
                                                                                                        P-PSDB; ADR14217
                                                                                                                                      WPI; 2004-562168/54.
                                                                                                                                                                                                                                                                                                                                   14-JAN-2003;
12-MAY-2003;
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                                                                                                                                                                                                       Neubauer MG,
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2003US-0469757P.
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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antiinflammatory, creebroprotective, vasotropic, immunosuppressive or wilnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions conditions of diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder and immune disorder and inflammatory disorder and immune disorders, hodgkin's lymphomas, haematopoietic tumours, hyper-IgM cytostatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM cytostatic disorders, hospablasia, x-linked anhidrotic ectodermal dysplasia, x-linked anhidrotic cytodermal dysplasia, x-linked anhidrotic survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, cytomatorial sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper cytosis and transplant rejection, conditions, birth defects, necrotic lesions, wounds, cytostic subject to the novel association with the NF-kappaB pathway of the cytosis related to aberrant signal transplant encounters and the propagation in cells infected invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank. Claim 1; diseases associated with NF-kappaB pathway. SEQ ID NO 217; 237pp; English.

Sequence 2003 B₽; 667 A; 324 C; 406 G; 606 Τ, 0 U; 0 Other;

US-10-627-571-2 (1-188) x ADR14216 (1-2003) Query Match: Best Local Similarity: Alignment Scores: Percent Similarity: 950.00 99.47% 98.94% 98.75% 1.27e-97 Matches: Conservative: Mismatches: Indels: Gaps: 2003 186 1 0 0

밁 ş 문 Ş 밁 Ş 밁 Ş 밁 á 밁 S S 141 121 101 444 384 324 264 204 18 61 41 21 μ LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla ATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAG GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCT CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG 160 40 140 100 623 563 120 503 443 80 383 60

248 GTGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG 307

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Percent Similarity:
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                                            US-10-627-571-2 (1-188)
                                                                                                                                                                                          The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (ii) for screening of evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining carcinoma associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of sequence. Note: This patent is an equivalent to basic patent CA gene useful as markers of usefunce. Note: This patent is an equivalent to basic patent.
                                                                                                                                                                       Sequence 2034
                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant nucleic acid useful for diagnosis and treatment comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                 inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atheroselerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; HIV propagation; gene; ds; human.
   13-JAN-2004; 2004WO-US000798.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC This invention relates to the novel association of protein sequences (and CC the genes which encode them) to the NF-kappaB pathway. The invention may CC be useful for the production of compounds with an antiinflammatory, CC cytostatic, hepatchropic, virucide, antiarthritic, antiineumatic, CC gastrointestinal-Gen, antiasthmatic, antiarthritic, antiineumatic, CC immunomodulator, cerebroprotective, vasotropic, immunosuppressive or cultivity or for gene therapy. The proteins and nucleotides are CC useful for diagnosing, preventing, treating, or ameliorating conditions CC or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder and condition is an CC immune disorders. Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atheroselerosis, cachexia, euthyroid sick Syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, corporations, disorders related to aberrant signal transplant crysction, conditions related to aberrant signal transplant conditions. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the convention. Note: This sequence does not appear in the specification but CC was obtained by the indexer from General association but
                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2081 BP; 668 A; 359 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
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12-MAY-2003; 2003US-0469757P
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                                                 The present invention relates to novel DNA and protein sequences which CC are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of CC a bioactive agent capable of modulating the activity of CAP; (iv) for cevaluating the effect of a candidate carcinoma drug; (v) for diagnosing CC carcinoma; (vii) for unhibiting the activity of CAP; (vii) for treating CC carcinoma; (viii) for neutralizing the effect of CAP; (vii) as a biochip; CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for CC determining Carcinoma Associated (CA) gene copy number. In addition, the CC carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent CC US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 496; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genomic sequence hCG36837
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Sequence 58723 BP; 16891 A; 11477 C; 12539 G; 17816 T; 0 U; 0 Other;

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RESULT 10
AAX98013
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XX AAX98
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                                                                                     Human; secreted protein; cancer; tumour; developmental abnormality; foetal deficiency; blood disorder; immune system disorder; inflammation; autoimmune disease; allergy; Alzheimer's disease; cognitive disorder; schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder; atherosclerosis; diabetes; cardiovascular disorder; kidney disorder; digestive disorder; endocrine disorder; infection; AIDS; ss.
 24-JUN-1999
                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                 by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumours, developmental abnormalities and foetal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences given in AAX97917 to AAX97315 and AAY36223 are used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAX99916 to AAX98029 represent 110 isolated human secreted protein genes. AAY36727 to AAY36727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 330; 537pp; English
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Kyaw H, Wei
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                                                     GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
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Wei Y, F
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ge capability; fat content; nutritional component; ds; gene; human.
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New secreted HKABT24 nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
                                                                                                                                       Claim
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identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other nutritional components. The present sequence represents cDNA encoding a novel human secreted protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at The invention relates to an isolated HKABT24 nucleic acid molecule. The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders. The nucleic acids are also useful for chromosome Sequence 1943 seqdata.uspto.gov.uk/sequence.html?DocID=20030055236 BP; 629 A; 325 ç; 399 G; 586 Ή. 0 U; 4 Other

Query Match: DB: Percent Similarity: Best Local Similarity: US-10-627-571-2 (1-188) x ADA11570 No.: 2.06e-97 948.00 98.94% 98.94% 98.54% 9 (1-1943)Length:
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The invention relates to 592 new human secreted polypeptides useful for CC diagnosing, treating or preventing e.g. immune disorders, inflammatory CC conditions, respiratory disorders, cancers, CNS disorders, or CNS disorders, or convergence at least 95% identical to the new sequences. The polypeptides, CC antibodies or antibody fragments that bind to the polypeptides, nucleic CC acids encoding the polypeptides, agonists or antagonists that binds to CC the polypeptide, are useful in preparing diagnostic or pharmaceutical CC compositions for diagnosing, treating or preventing an e.g. immune CC disorders, inflammatory conditions (e.g. inflammatory bowel disease, CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and CC e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative CC disorders (e.g. parkinson's disease or Alzhaimer's disease), and CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The CC polynucleotides are useful for chromosome identification, chromosome CC mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therapy, for identifying individuals from minute biological samples, in forensic biology, and as hybridization concerns the polypeptides are useful for as molecular weight markers on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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P-PSDB; ADA57137.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cardiovascular; antiarteriosclerotic; gene therapy; human secreted protein; immune disorder; inflammation; respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; SEQ ID NO 430; 1754pp; English.
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RESULT 13
ACN44177
ID ACN44
XX ACN44
XX ACN44
XX IB-NC
DT 18-NC
DX MOUSE
XX MOUSE
XX Cytos

ACN44177 standard;

CDNA;

2087 BP

Cytostatic;

carcinoma; lymphoma; cancer; murine;

gene;

gb

ACN44177; 18-NOV-2004 Mouse mRNA

sequence

(first

entry)

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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to a gene encoding one of the polypeptide of the invention. Note: The sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1943 BP;
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                            LysMetLeuAspGluGluAsnIle 188
                                                                                   LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                                                               SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
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                                                                                                                                                                                                                                                                           MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                                                                            TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of binding to Carcinoma Associated protein (CAP); (iii) for screening of binactive agent capable of binding to Carcinoma Associated protein (CAP); (iii) for screening of a binactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) for treating; (x) for diagnosing carcinoma are uncommana or a propensity to carcinoma; and (xi) for determining Carcinoma and (CAP) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent US2002182586AI, for which no segmence data was analyzed.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2087 BP; 556 A; 487 C;
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                                                                                                                                                                                                         LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                                                                                                                       GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                                                                                  GTGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
                   MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                            PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAla
                                                                                                                         GTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAG
                                                                                                                                                                                     CTAGATGAGCTGTACAGGGTGACCAAGGAGTACACCCAGAACAAGAAGGAGGCGGAGAGG
                                                                                                                                                                                                                                                   GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCAGCGAGGTG
ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid useful for diagnosis and treatment of carcinoma nucleotide sequence.
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RESULT 14
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Alignment
                                                   The present invention relates to novel DNA and protein sequences which CC are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for condition of determining Carcinoma associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent.
                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACN44176;
                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                              Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002; 2002US-00087192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
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                                                                                                                                                                                                                                                                                 SEQ ID NO 493; Opp; English.
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                                                                                                                                                                                                                                                                                                               a nucleotide sequence
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Best Local Similarity: Query Match: DB:

Score:

No.:

.97e-92

Percent Similarity:

2.97e-9 920.00 98.94% 94.15% 95.63%

Mismatches: Indels: Gaps:

62231 177 9 2 0

Matches: Conservative: Length:

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RESULT 15
AAH07403
ID AAH07
XX AAH07
XX AAH07
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX EP107
PN EP107
PD 07-FE
XX 29-JU
PR 27-JU
XX 29-JU
PR 11-JF
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  Ota T,
Ishii S,
                                                                                                                         29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA clone (5'-primer)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; primer;
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  Isogai T,
, Sugiyama
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  Nishikawa T,
T, Wakamatsu
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Hayashi K, S
1 A, Nagai K,
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  Saito K,
Otsuki
                       Yamamoto J;
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WPI; 2001-318749/34.

Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length

Claim 1; SEQ ID NO 4238; 2537pp + Sequence Listing; English

CC length cDNAs defined in the specification. Where a primer set complementary to the CC complementary strand of a polynucleotide comprises one of the 5602 cc nucleotide sequences defined in the specification, where the CC onligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end' cc sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC specification. The primer sets can be used in antisense therapy and in the specification. The primers are useful for synthesising polynucleotides, cgene therapy. The primers are useful for synthesising polynucleotides, comparticularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and compared the proteins encoded by compassing the primers allow obtaining of the full-length cDNAs and proteins encoded by compassing the proteins are also useful for the compassing compassing the proteins and compassing of the full-length cDNAs and proteins encoded by compassing the proteins are also useful for the compassing compassing compassing the proteins encoded by compassing co invention describes primer sets for synthesising 5602 full-

Sequence 816 BP; 262 A; 155 Ç; 180 છ 212 Τ, 0 u; 7 Other;

Percent Similarity:
Best Local Similarity:
Query Match: Score 2.81e-94 916.00 97.89% 96.84% 95.22% Conservative: Mismatches: Indels: Length: Matches: 816 184 2 2 2 0

US-10-627-571-2 (1-188)x AAH07403 (1-816)

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121 LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 	101 MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg	81 PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla 	61 LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln 	41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys 	21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal 	1 MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
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                           gene expression (comprising a plurality of single exon nuclear and probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORP-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records cited above in the expression of a single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe the hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human centered to the string of the string human centered to the stri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alternations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 22914; 80pp; English
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alternative splicing event; genomic alteration.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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The probe,

methods and apparatus are useful

ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;

Novel human cDNA sequence #269

07-OCT-2004

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2003;
09-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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GTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGCAT
                                                                AspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrVal
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                                                GAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCATT
                                                                                                                                               Sugiyama T,
, Isono Y,
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RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide and polypeptide useful for diagnosing, preventing treating conditions such as neurodegenerative diseases, anemias, play disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases of the conditions of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang TY, Zhang J,
Zhou P, Ghosh M,
Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective; antianaemic; anticoagulant; thrombolytic; vn antiulcer; osteopathic; immunosuppressive; antiinflammatory; gene therapy; chromosome 15q21.2; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease neurodegenerative diseases; anaemia; platelet disorder; wound; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; no
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30899) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention; a method of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The invention further discloses methods of poventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes and/or monoclonal antibodies for carrying out the methods of the

Claim 1; SEQ ID NO 851; 1185pp; English

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US-10-627-571-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention; methods for the identification of compounds that modulate the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the cDNA sequences of the invention CC (ADC31861-ADC32627) and the polypeptides encoded by the contigs (ADC32628 ADC3394). The nucleic acids and polypeptides of the invention are useful in diagnostics, drug screening, forensics, gene mapping, in the cidentification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of data and products dependent on NNA and amino acid sequences. They are also used for treating diseases such as Parkinson's disease, Alzheimer's cidenater. The nucleic acids may also be used as hybridisease or concer. The nucleic acids may also be used as hybridiseation probes or concer. The nucleic acids may also be used as hybridisetion probes or crimers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, can as food supplements. The present sequence represents a specifically claimed human cDNA sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was for the print of the printed specification.
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RESULT 19
ACH92216
ID ACH92
    The invention relates to a nucleic acid probe for measuring human gene compression, comprising any of the 27,400 fully defined nucleotide encoding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification. The probe is a single exon probe that chybridises under high stringency conditions to a nucleic acid molecule cather shall be set of single exon nucleic acid probes for measuring human cells or tissues. Also included are a spatially-cather shall be expressed in human cells or tissues. Also included are a spatially-cather shall be expressed in plurality of single exon nucleic acid probes for measuring human gene expression, a method of gene expression (comprising a plurality of single exon nucleic acid caid cand addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, that binds specifically to a peptide cited above, an ORP-encoded peptide exon probes or microarrays to cather a string to measure gene expression, a method of providing thuman gene expression data by subscription, and a computer-readable cated above. The probe, methods and apparatus are useful in gene captesion analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, the probes are used in identifying and characterising calternative splicing events, in detecting and characterising gross calternative splicing events, in priming the synthesis of nucleic acids, or in expressing the ORP-encoded peptide. The present sequence is a human calcider this patent did not form part of the printed specification, but was obtained calternated and out the printed specification.
patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; probe; ss; gene expression; single exon probe; microarray;
alternative splicing event; genomic alteration.
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                                   Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangictasia; leukodystrophy; anxiety; pain; obesity. Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; cell differentiation; cell proliferation; haematopoiesis; wound healing;
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Kekuda R, Gerlach VL; a R, Pena CEA;

WPI; 2002-713508/77. P-PSDB; ABG97498.

New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or parkinson's disease. multiple

Claim 22; Page 139; 266pp; English

The present invention relates to a new polypeptide (NOVX). The NOVX CC polypeptide, nucleic acid and antibody are useful in the manufacture of a comedicament for treating a syndrome associated with a human disease, CC preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or CC diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau CC syndrome, Alzheimer's disease, stroke, tuberous sclerosis, erebral cpalsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-cc telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, inferrility, inflammatory bowel disease, atherosclerosis, hypertension, cc scleroderma, haemophilia, diabetes, pancreatities, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and cpolypeptides may also be used as targets for the identification of small cdifferentiation, cell proliferation, hematopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind continuouspecifically to NOVX substances for use in therapeutic or cdiagnostic methods. The nucleic acids are further used as hybridisation content of the invention. The present nucleic acid sequence encodes a human NOVX protein of the invention.

Sequence 619 BP; 97 P 219 ü 207 ç 96 H .. 0 ď;

Homo sapiens

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RESULT 21
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tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression;
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Sequence 645

BP; 97

A; 228

C; 219

G; 101

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U; 0 Other;

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cc syndrome, Alzheimer's disease, stroke, tuberous sclerosis, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, erebral cpalsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-cc palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-cc infertility, inflammatory bowel disease, inflammatory bowel disease, inflammatory bowel disease, coresis, inflammatory bowel disease, atherosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and core polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell griderentiation, cell proliferation, haematopolesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or chiaminospecifically to NOVX substances for use in therapeutic, and probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present nucleic acid sequence encodes a human NOVX protein of the invention
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                                                                                                                                                                                                                                                                                                                                                    medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, prefypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atheroselerosis, cancer, infections, osteoporosis or parkinson's disease.
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02-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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P-PSDB; ABG97497.
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31-OCT-2001;
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tturajan M, Gusev VY, Keku
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                                         Antiarteriosclerotic; cytostatic; HIV; antiallergic; antianaemic; antiarteriosclerotic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia; Parkinson's disease; epilepsy; stroke; knockin humanised animal; transgenic animal; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                              Human secreted protein DNA SEQ ID
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Query Match:
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                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                        Alignment
                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated human secreted protein (SECP)

CC polypeptide from 63 fully defined protein sequences given in the

CC specification. The polypeptide is useful for the diagnosing/treating of a

CC disease with decreased/overexpression of SECP. Examples of disorders

CC associated with abnormal expression of SECP include a cell proliferative

CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory

CC disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.

CC congestive heart failure, ischaemic heart disease; developmental disorder e.g.

CC congestive heart failure, ischaemic heart disease; developmental disorder e.g.

CC renal tubular acidosis, hypothyroidism, neurological disorder e.g.

CC Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.

CC The SECP polymuclectide and polypeptide are further useful for analysing

CC the proteome of a tissue or a cell type. The polymuclectide is useful for

CC creating knockin humanised animals (plgs) or transgenic animals (mice or

CC rats) to model human disease, and for somatic or germline gene therapy,

CC and further for generating hybridisation probes useful in mapping the

CC raturally occurring genomic sequence. This polymuclectide sequence

CC represents the DNA of a human secreted protein of the invention
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21-NOV-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted proteins and polynucleotides for diagnosing, preventing disorders of cell proliferative, cardiovascular, developmental, neurological and autoimmune/inflammatory disc
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P-PSDB; AAO21665.
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09-NOV-2000;
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Ila M, Thornton M, Elliott VS,
Hafalia AJA, Tang YT, Bandmar
Thangavelu K, Lee S, Xu Y, Y
Duggan BM, Sapperstein SK;
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GATGAGCTGTACCGCGCCACCAGGGAGTTCACGCCGCAGCCGCAGGAGGCCCAGAAGATG
                   AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
                                                          AAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGATGACACCAGCAGTGAGGTGCTG
                                                                              GCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAGAAGAAGCTCCTGAGT
                                                                                                                                 AlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGly
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; 2000US-0248642P.
; 2000US-0249824P.
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Thornton M,
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Indels:
Gaps:
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Lu Y, Gietzen
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chell CD;
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising; (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region c (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3 a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour-associated antigenic target (TAT) cDNA sequence #2473.
                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule and encoded polypeptide, i preventing or treating cell proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-534300/51.
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                                                                                                                                                                                                                                                                                                                             Claim 1;
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; cell proliferative disorder; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                     for diagnosing, such as cancer.
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cc length coding region of the above nucleotide sequences; or (c) a sequence (c) length coding region of the above nucleotide sequences; or (c) a sequence (c) at least 80% identical to (a) or (b); (5) a chimeric polypeptide (c) an isolated antibody that binds to the above polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (10) a cc composition of matter comprising the above (c) polypeptide; (10) a cc composition of matter comprising the above (c) polypeptide; (10) a cc composition of matter comprising the above (c) polypeptide; (10) a cc composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of cell is at least in part dependent upon a growth of the cell is at least in part dependent upon a growth of cell is at least in part dependent upon a growth of cell is at least in part dependent upon a growth of described above; (15) methods of distancer of containing the protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a contain, and (17) a method of binding an antibody, oligopeptide or companic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, gene therapy. The composition and methods are useful for diagnosing, cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.
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Sequence 2186 478 A; 624 ü 673 G: 411 T; 0 U; 0 Other;

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Query Match:
              Best Local Similarity:
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4.69e-57
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61.64%
      Length:
Matches:
Conservative:
Mismatches:
Indels:
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2186
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US-10-627-571-2 (1-188) x ADQ85659 (1-2186)

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CACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGACTGCGACTTCCTGGCTGCGCTC
                                                              CTGCTCGAGTGCCGCGACCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCC
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                                                                                      LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
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               CC target (TMT) nucleic acid (comprising: (a) any of 4622 nucleotide
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%
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                                                                                                      ADQ84271 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCAAGAACCTGGTCAAGGTGGCCCTGAAGCTGGGACTGCTGCTGCGTGGGGACCAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAGAAGAAGCTCCTGAGT
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                                                                                                                                                                 ATGCTGGACGAGGGCAGCCTC
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593.00
79.14%
56.68%
61.64%
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Human tumour-associated antigenic target

(TAT) cDNA sequence #1085

07-OCT-2004

(first entry)

292

41

232

412 101 352 81

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Percent Similarity:
Best Local Similarity:
                                                                                                                                                                            CC target (TAXT) mucleic acid comprising: (a) any of 4622 nucleic defect (TAXT) mucleic acid complement of (a) or (b); (d) a sequence that has 80%; (c) the complement of (a) or (b); (d) a sequence that has 80%; (e) complement of (a) or (b); (d) a sequence that has 80%; (e) complement of (a) or (b); (d) a sequence that has 80%; (e) complement (c) and the process of complement (c) and expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) cc a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-comprising the above polypeptide; (b) an isolated encoded by the full-comprising the above polypeptide fused to a heterologous polypeptide; (6) can isolated antibody (b) an isolated oligopeptide; (f) a process cc for producing the antibody; (b) an isolated oligopeptide; (7) a process cc for producing the antibody; (b) an isolated oligopeptide; (f) a composition of matter comprising organic molecule that binds to the above polypeptide; (f) a composition of matter contained within the container; (10) a composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of cinhibiting the growth of a cell that expresses the above protein, where the composition of methods of disposition and method of determining the protein in a sample suspected of containing the protein in a sample suspected of containing the protein described above; (15) methods of disposition of a cell that expresses the above protein in a containing the protein and contained and containing the protein and contained and containing the protein and contained and contained and contained containing the protein and contained contained containing the protein and contained containe
                                                                                                                             Alignment
                                                                                                                                                                                                                       a medicament for the therapeutic treatment or diagnostic cell proliferative disorder or cancer. The present sequent human TAT cDNA sequence from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes an isolated tumour-associated antigenic nucleic acid comprising: (a) any of 4622 nucleotide
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     4.69e-57
593.00
79.14%
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Matches:
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                                                                                                                     29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA clone (5'-primer)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-2001
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                                                                                            99JP-00300253.
2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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     Nishikawa
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  Hayashi K,
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     Saito
  ζ,
     Yamamoto
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence)3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03165 to AAH13628 and AAH13632 to AAH3742 represent human cDNA sequences; ABB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent controlleds, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                              LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
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LeuLeuAsnGluCys-ArgGluMetLeuHisGln 131
                                                 ATGACCGTGGNCAGTTTCCAACAAGGGGGGTTATACCTTTGACCGGAATGTGTTATCCAAG
                                                                                                                                                     TTTAATCAAGATGAGCTAGCATTGATGGNGAAATTTAAGAAGAAAGTTCATCAGCTTGCT
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Best Local Similarity: Percent Similarity:

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                                                                                                             and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for tissue regeneration, for wound healing and in the treatment of burns, incisions and ulcers. The proteins are also useful for regulating haematopoiesis and for treating myeloid or lymphoid cell deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                    proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treat immune deficiencies and disorders such as autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coagulation disorder; inflammatory disorder; Crohn's disease; incision, tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to 592 polynucleotides which have been derived a variety of human tissue sources and which encode novel secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer;
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The invention relates to human secreted polypeptides designated LP095, LP219, LP220, LP221, LP222, LP237 or LP238 and nucleic ac molecules encoding such polypeptides. Novel secreted proteins of the invention are used for treating diseases such as atherosclerosis, Alzheimer's disease, diabetic retinopathy, psoriasis, pancreatitis, arteriosclerosis, rheumatoid arthritis, colorectal adenomas, severe combined immunodeficiency, ischaemia, carcinomas, haemolytic anaemia, reperfusion injury, neoplasms and cancer especially liver cancer. They are also used for wound healing. Polynucleotides of the invention can it used to generate transgenic animals or knock out animals, which in turn are useful in the development and screening of therapeutically useful reagents for use in the treatment of diseases associated with LP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 140-141; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel proteins and polynucleotides of secreted proteins useful for treating various diseases e.g. rheumatoid arthritis, cancer, psoriasis, diabetic retinopathy, arteriosclerosis, ischemia or reperfusion injury.
                                                                                        polypeptide associated activity. They are also used in gene present sequence is human LP237 secreted protein encoding c
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BP; 305 A; 319 C; 312 G; 229
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US-10-627-571-2 (1-188) x AAD38699 (1-1165) 6.34e-50 527.00 77.22% 55.00% 54.78% Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1165 99 40 39 1

26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr :::|||:::|| GlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeuAspGlu CGCCACGTGTTTGATCACTTCTGACCCAGGTCTGCTCACGGCCCTCTATGGGCCT---AsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsnProPhe ATCAPAGTGGCCATCAAGGTGGCTGTGTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGCAGAAGAAGCTACTGAGTAAGATGGCGGGT PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer ArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgVal PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys LeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrValValSer IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu CGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC CGGGATGTGCTGCTAGAGTTGGTGGAACACCÁCCTCÁCGCCCAÁGTCÁCATGGCCGCATC CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCCAGCGCGTGATCAAGGACCTG 165 145 185 45 168 125 408 105 65 25 585 528 468 348 85 288 228

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                                 Percent Similarity:
Best Local Similarity:
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CARZI2066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The encoded polypeptides (ABP68902-ABP68949) are useful as molecular weight markers, as a food supplement, for generating antibodies, in medical imaging, screening and diagnostic assays and for treating cell-proliferative disorders (cancer), neurodegenerative diseases (Parkinson's proliferative disorders (cancer), neurodegenerative diseases (Parkinson's Alzheimer's disease), autoimmune diseases (multiple sclerosis, cliabetes, lupus) genetic disorders, myeloid or lymphoid disorders, liver platelet or coagulation disorders, wound, burns, incision, ulcers, liver or lung fibrosis, infections (bacterial, viral, fungal, parasitic), arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format and directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection, arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidiabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated
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proliferative disorder; neurodegenerative disease; bacterial;
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T, Wang J, War
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Wa Y, Yamazaki V, Chen
, Wang D, Drmanac RT;
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05-MAR-2002; 2002WO-US005095
20-AUG-2002; 2002US-00225251
                              WPI; 2004-238579/22
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                                                                                                                                             (TANG/) TANG Y T. (XUEA/) XUE A. (DRMA/) DRMANAC R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel human arginine-rich protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated arginine-rich protein-like polynucleotides and polypeptides, useful for diagnosing and/or treating conditions associated with aberrant activity of the arginine-rich polypeptides, such as cancer and
                                   24-APR-2001
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                                                                                                 AAF59594 standard;
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Human cell cycle and proliferation

protein CCYPR-5 cDNA,

SEQ ID NO:59.

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LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr 45

PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer 25

TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGGAGAAGAAGCTACTGAGTAAGATGGCGGGT 171

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US-10-627-571-2 (1-188)

x AAF59594 (1-1268)

Percent Similarity: Best Local Similari Query Match:

Similarity:

Conservative: Mismatches: Indels:

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decreased expression of functional CCYPR, while CCYPR are used to treat diseases or conditions associated with overexpression of functional CCYPR, while CCYPR antagonists are used to treat diseases or conditions associated with overexpression of functional CCYPR. Monoclonal or polyclonal antibodies to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunosasys to detect CCYPR. CCYPR itself may be used to detect compounds e.g., antibodies, oligonucleotides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that modulate the activity of CCYPR. CCYPR mucleotides can be used to generate transgenic animal models of human disease, and can be used in gene therapy in target cells with genetic abnormalities with respect to the expression of CCYPR. Diseases which can be diagnosed, treated and creased using CCYPR. Diseases which can be diagnosed, treated and compounded immune, developmental and cell signalling disorders, and cell proliferative disorders including cancer. Specific examples of these disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, and cell anaemia, disorders of the menstrual cycle and
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08-SEP-1999;
10-NOV-1999;
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P-PSDB; AAB60457.
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                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequences AAF59590-AAF59643 represent cDNAs encoding 54 human cell cycle and proliferation proteins (CCYPR), AAB60453-AAB60506. CCYPR and agonists
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                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
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                                     Drosophila; devipharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4406 BP; 1178 A; 1021 C; 1027 G; 1180 T; 0 U; 0 Other;
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genes from Drosophila
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TCCATCATATCATTCTACGAAGTGGACTTCACGTTCGACCTGCCGTACCTGCAAAAGTCA 1205
                                                                                                                                                                                 CTGATCAAGAACATCATCAAGATTGTGATCAAGATCGGTGTGCTCCACCGGAACAATCAG
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                          ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
                                                          TTCAGCGACGAGCTGCAGAAGGCGGAGCTCTTTAAGAGAAAGTTTCAAGTGAGTCTT
                                                                                                                                                 PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLys----------
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                       for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                           are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing blodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR,
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide comprising any one 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding a reading frame of the novel polynucleotide. The nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide sequences obtained from various cDNA libraries, as hybridization probes, as oligomers for PCR, for chromosome and gomapping, in the recombinant production of protein, or in generating
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                                        New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome derived single exon probe #9211.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
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||||:::|||||:::||||||:::||||||:::|||
TCAGCTCAAAGAGCCTGGCACTGCAAGCAAGAAGAAGCTACTGAGTAAGATGGCGGGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PheHisGlnValAspTyrThrPheAspArgAsnValLeuSer 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAlaMetThrValValSer 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTGGTGAGGTAGACTTCACCTTCGAGGCTGCTGTTCTGGCT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
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                                                                                                                                                                                                   Rank DR,
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324.00
78.95%
54.39%
33.68%
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Matches:
Conservative:
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Indels:
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Claim 15; SEQ ID NO 9211; 80pp; English
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CC measuring human gene expression, a vector comprising the single exon CC probe cited above, an ORF-encoded peptide comprising the single exon CC contiguous amino acids of any of the above- mentioned amino acid CC sequences (optionally with conservative amino acid substitutions), an CC methods of selling and/or licensing single exon probes or microarrays to centhods of selling and/or licensing single exon probes or microarrays to CC a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable contrage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene cappression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. CC In addition, the probes are used in identifying and characterising craliferations, in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, cor in expressing the ORF-encoded peptide. The present sequence is a human construction of the printed specification, but was obtained contained and the contained across the contained across of the printed specification, but was obtained contained across the contai gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid. sequences fully defined in the specification. The probe is a single exon probe that seqdata.uspto.gov/sequence.html?DocID=20030194704

 $\begin{array}{c} \mathsf{w} \times \mathsf{o} \\ \mathsf$

Sequence 500 BP; 164 A; 71 Ç 107 G; 158 Ή, 0 Ç, 0

Percent Similarity: Best Local Similari Query Match: Similarity: 4.25e-25 304.00 100.00% 100.00% 31.60% Mismatches: Indels: Conservative: Length: 0 0 0 5 50

134 GlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSer 123 174 154 AspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPheLysProHisLeuGln 63 ω LysLeuCysAspGlyIleAsnLysMetLeuAspGluGluAsnIle 188 GATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAA CAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCA

173

62

122

153

밁 Ś 뮹 Ś

US-10-627-571-2 (1-188) x ACH76016

(1-500)

AAH04721 RESULT 36

밁 S

AAH04721 standard; CDNA; ВP

******* AAH04721;

26-JUN-2001 (first entry)

CDNA clone (5'-primer) SEQ ID NO:1556.

Human; primer; detection; diagnosis; antisense therapy; gene therapy; 88

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                                                                                                                                                                                     US-10-627-571-2 (1-188) x AAH04721 (1-714)
                                                                                                                                                                                                                         Query Match:
DB:
                                                                                                                                                                                                                                                            Best Local Similarity:
                                                                                                                                                                                                                                                                                Percent Similarity:
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                       sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at 1-s nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5600 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ota T,
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-2000; 2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length cDNAs defined in the specification. Where a primer set comprises:
                                                                                                                                                                                                                                                                                                                    No.:
                                                                         124
                                                                                                                                            104 ValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsn
                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isogai T,
Sugiyama
ArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyrAsn
                                                                     GluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1556; 2537pp + Sequence Listing; English
                                  GAGTGCCGCGACCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCCACGGC
                                                                                                            GTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGCGTGCTGGCCGCCGGGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                        BP;
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                                                                                                                                                                                                                                                                                                                                                                        113 A; 246
                                                                                                                                                                                                                                       1.56e-23
292.00
81.18%
58.82%
30.35%
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T, Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                        203
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A, Nagai K,
                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                             Matches:
                                                                                                                                                                                                                                                                                                                                                                        G; 148
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Otsuki
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50
19
16
0
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                                                                       143
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        CC length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide which complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602

CC oligonucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC oligonucleotide comprising a sequence complementary to the

CC onplementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide which comprises a 3'-end sequence, where the

CC oligonucleotide comprises a 1'-end sequence, where the

CC oligonucleotide which comprises a selected from those defined in the

CC offication. The primer sets can be used in antisense therapy and in

CC gene therapy. The primers are useful for synthesising polynucleotides,

CC oparticularly full-length cDNAs. The primers are also useful for the

CC detection and/or diagnosis of the abnormality of the proteins encoded by

CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893

CC present human amino acid sequences, and AAH13629 to AAH3632 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis of the abnormality of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T, 1
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human cDNA sequence SEQ ID NO:18986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH18715
                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 18986; 2537pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-2000; 2000EP-00116126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH18715;
                                                                                                                                                                                                                                                                                                                                                             The present invention describes primer sets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMetLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugiyama
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2000JP-00118776.
2000JP-00183767.
2000JP-00241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA; 1602 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wakamatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagai K,
                                                                                                                                                                                                                                                                                                                                                              for synthesising 5602 full-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Otsuki T;
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RESULT 38
AAK56622
ID AAK56
XX AAK56
XX O6-NC
XX O6-NC
XX CYCOS
XX CYCOS
XX O7-NS
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
                   31-JAN-2000

04-FEB-2000

04-FEB-2000

02-MAR-2000

16-MAR-2000

17-MAR-2000

18-APR-2000

19-MAY-2000

07-JUN-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

11-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune/haematopoietic antigen encoding cDNA SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune; haematopoietic; immune/haematopoietic antigen; cancer;
aric; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCCACGGC
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                   2000US-0179065P.
2000US-0184664P.
2000US-0184664P.
2000US-0184654P.
2000US-0199074P.
2000US-0199123P.
2000US-0205515P.
2000US-0204867P.
2000US-0214886P.
2000US-0215135P.
2000US-0216847P.
2000US-0216849P.
2000US-0217487P.
2000US-0217487P.
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292.00
81.18%
58.82%
30.35%
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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   14-AUG-2000
18-AUG-2000
18-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
01-SEP
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14-AUG-2000;
14-AUG-2000;
2000US-0224519P.
2000US-0225214PP.
2000US-022526PP.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225758P.
2000US-0225759P.
2000US-022668BP.
2000US-02270182P.
2000US-02270182P.
2000US-0229349P.
2000US-0239344P.
2000US-0239344P.
2000US-0239344P.
2000US-0239344P.
2000US-0231244P.
2000US-0231249P.
2000US-0231393P.
2000US-0241786P.
2000US-0241786P.
2000US-0241809P.
2000US-0246474P.
2000US-0246474P.
2000US-0246477P.
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amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK67694 represent human immune/haematopoietic antigen genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
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17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                        Nucleic
                                                                                                                                                                                                                                                                                               P-PSDB; AAM83841
                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN
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7-NOV-2000;
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7-NOV-2000;
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                                                                                                                                                                                                                                                       c acids encoding for preventing.
                                                                                                                                                                                                 to AAK64702 encode the human immune/haematopoietic antigen
                                                                                                                                                                                                                                SEQ ID NO 1682;
                                                                                                                                                                                                                                                                                                                                      Barash SC,
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2000US-0246532P.
2000US-0246532P.
2000US-0246613P.
2000US-0246611P.
2000US-024920P.
2000US-024920P.
2000US-0249211P.
2000US-0249214P.
2000US-0249214P.
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2000US-024926P.
2000US-024926P.
2000US-024926P.
2000US-024928P.
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2000US-0256719P.
2000US-0251479P.
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2000US-0250160P.
2000US-0250391P.
2000US-0251030P.
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2000US-0251990P
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2000US-0251868P.
2000US-0251869P.
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2000US-0246525P.
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  the present
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3-0246523P.
                                                                                                                                                                                                                                                                                                                                                                SCI
                                                                                                                                                                                                                                                      human immune/hematopoietic diagnosing and/or treating
                                                                                                                                                                                                                                                                                                                                      Ruben SM;
                                                                                                                                                                                                                             3071pp + Sequence Listing;
    invention.
  AAK54942 to
antigen genomic
AAK54950 and AAM82169
                                                                                                                                                                                                                                                       antigen polypeptides, cancers and metastasis.
                                                                                                                                                                                                                              English.
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and

the

Claim 1; SEQ

ID NO 14427;

71pp + Sequence Listing; English

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RESULT 39
AAC10352
ID AAC10
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DB:
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                                                                        WPI;
                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 441
                                      New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                           21-FEB-2000; 2000EP-00200610
                                                                                                                                                                                                    EP1033401-A2
                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                   06-OCT-2000
                                                                                                                                                                                                                                                                                                                                            AAC10352 standard; cDNA; 340
                              diagnostic,
                                                                                            Dumas Milne Edwards
                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                        AAC10352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                 (GEST ) GENSET
                                                                                                                                                                                                                                            therapy;
                                                                       2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity:
                                                                                                                                                                                                                                                                              secreted
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                                                                                                                                                                                                                                                                                                                                                                                     TTGGT-GAAGTNGATTTCACT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                  PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeu :::||||||:::||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGCCCTGGCTAMCCGCTTTCGCCAGAARCTGCGGCAAGGTGCCATGAMGGCATTGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleLysThrValIleLysLeuAlaIleLeuTyrArgAspAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCAGCGCGTGATCAAGGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAAGAAGCTACTGAGTAAGATGGCGGGT
                                                                                                                                                                                                                                                          EST;
                              forensic,
                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 99
                                                                                                                                                                                                                                              chromosome mapping;
                                                                                                                                      99US-0122487P
                                                                                                                                                                                                                                                                            protein 5'
                                                                                                                                                                                                                                                          expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.47e-22
281.00
74.36%
51.28%
29.21%
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                            gene therapy and
                                                                                            Duclert
                                                                                                                                                                                                                                                          sequence
                                                                                                                                                                                                                                                                              EST,
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                                                                                                                                                                                                                                                                                                                                            ВP
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                                                                                                                                                                                                                                                                             SEQ ID NO: 14427
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                        tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 89
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                                                                                            Giordano
                            chromosome mapping procedures
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                                        tag (5' EST) for to 5'ESTs and fo
                                                                                                                                                                                                                                                          cDNA isolation;
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RESULT 40
AA192435/c
ID AA1924:
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XX AA1924:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                  28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing
                                                                  P-PSDB; AAO12504
                                                                                             WPI; 2001-514838/56.
                                                                                                                                                                                                                                                                                                                                                      26-FEB-2001; 2001WO-US004927
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTG
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                                                                                                                                                      Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.44e-19
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94.55%
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ID AAC10
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XX Homo
XX Gene
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production of other cytokines in other cell populations. The polypucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/ninhbin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                Human; 5' EST;
gene therapy; 
                   Dumas Milne Edwards
                                                                                                                                                                                   EP1033401-A2
                                                                                                                                                                                                                                                                                                  Human secreted protein 5' EST,
                                                                                                                                                                                                                                                                                                                                                                      AAC10359;
                                                                                                                                                                                                                                                                                                                                                                                                      AAC10359 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating trytokine, cell proliferation or cell differentiation or which may induce
                                                                                   26-FEB-1999;
                                                                                                                  21-FEB-2000; 2000EP-00200610
                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                     06-OCT-2000
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                                                  (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 AAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGATGACACCAGCAGTGAGGTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 GCCATGGACACCTTCAGCACCAAGAGCCTCTGCAGGCGCAGAAGAAGCTCCTGAGT 125
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                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                   chromosome
                                                                                   99US-0122487P
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206.00
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62.30%
21.41%
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                                                                                                                                                                                                                                                  mapping; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' most and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                   Human; probe; alternative sp
                                                                                                                                                                                                                                                                                                                             Human genome derived single exon probe #11708.
                                                                                                                                                                                                                                                                                                                                                                  29-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                               ACH78513 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 252 BP; 57 A; 88 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 14434; 71pp + Sequence Listing; English
WPI; 2004-119264/12
                                                           (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                         03-APR-2002; 2002US-00029386
                                                                                                                                                         03-APR-2002; 2002US-00029386
                                                                                                                                                                                        16-OCT-2003.
                                                                                                                                                                                                                       US2003194704-A1.
                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGAC
                             Rank DR,
                                                                                                                                                                                                                                                                               ss; gene expression; single exon probe; microarray;
splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                secretion vectors
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166.00
100.00%
100.00%
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                               Hanzel DK;
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Matches:
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Indels:
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gene expression analysis, for identifying or characterizing altern splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                               New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative
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Claim 15; SEQ ID NO 11708; 80pp; English

commeasuring human gene expression, a vector comprising the single exon contiguous amino acids of any of the above-mentioned amino acid soft contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an considered antibody that binds specifically to a peptide cited above, and constructive amino acid substitutions of acid single exon probe contain acid above. The probe, methods and apparatus are useful in gene capperssion analysis. The probes may be used as tools for surveying the superssion analysis. The probes may be used as tools for surveying the superssion acid substitution, the probes are used in identifying and characterising calternative splicing events, in detecting and characterising gross calternative splicing events, in detecting and characterising gross calternative splicing alternations, in priming the synthesis of nucleic acids, but account of the surveying the synthesis of nucleic acids. The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon mucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at Sequence 543 seqdata.uspto.gov/sequence.html?DocID=20030194704 BP; 137 A; 128 C; 119 G; 159 T; 0 U; 0 Other;

Percent Similarity: Best Local Similari Query Match: No.: Similarity: 2.4e-07 148.00 88.64% 54.55% 15.38% Length: Matches: Conservative: Mismatches: Indels: 543 24 15 0

US-10-627-571-2 (1-188) x ACH78513 (1-543)

밁 밁 S 밁 Ś AXU ADP04796 ADP04796 standard; cDNA; 1329 143 GlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyr 183 163 63 w LeuAspGluGlu 186 AGTCTGGATGGAGACTGTAGGCCCCAACCTCAAGAGGATTTGTGAAGGAATCAATAAGTTG AsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMet 182 CTAGATGAGAAA 134 GGGCGCATCAACCACGTCTTTAACCACTTTGCCGATGTGGAGTTCCTCTCCACCCTCTAT 122 62 162

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                                                                                                                                                                                                                                                                                                                                                                                                                                                      medicines and gene therapy techniques. Accordingly, they can be used in the research of various genetic diseases, as well as the analysis of cell proliferation, differentiation and reproduction. Furthermore, such compositions can be useful for environmental measurements and water surveys, particularly for sea water surveys, and also for the preparation of transformed sea squirt for improving edibility of sea squirt such as Halocynthia roretzi. This polymucleotide sequence is a sea squirt cDNA sequence that exhibits tissue specific expression during development,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  that are derived from the sea squirt Ciona intestinalis. Specifically, it refers to those genes that are expressed in the tissues or organs of the sea squirt during its developmental phase. The present invention describes the identification of these genes as useful for elucidation of these genes as useful for elucidation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel gene cluster which is specifically expressed in tissue or organ during developmental phase of sea squirt, useful for elucidation of mechanism of development of tissue or organ of sea squirt.
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ciona intestinalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the mechanism of development and hence for developing regeneration
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proliferation; differentiation; reprodu
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                                                                                  ValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeuIle
                                                                                                                                                     SerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyrArg
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                                                            CGTAAACAAACTGAAGCAAAGAAAGAAAAGAAAGAGAGAAAAGAAATGCTTAAA
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                    The present invention describes proteins and their fragments (I) encoded by chromosome 2 of the human malarial parasite, Plasmodium falciparum. Also described are: (I) nucleotide sequences (II) encoding (I), and (2) vaccines against P. falciparum infection comprising (I) or (II) (I) and (II) are useful for the development of vaccines against P. falciparum infection. (I) and polyclonal antisers or a monoclonal antibody raised to immunogens comprising the sequences of (I), are useful in the detection of infection with P. falciparum. Furthermore, (I) (especially when they are rifins or secreted or membrane proteins) can aid the identification
                                                                                                                                                                                                                                                                                                                                                            Proteins encoded by chromosome 2 of the human malarial Plasmodium falciparum, useful as antimalarial vaccines diagnosis of P.falciparum infection.
of drugs to treat or prevent P.
                                                                                                                                                                                                                                                                                                       Disclosure; Page 549-550; 577pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide new targets for vaccine and drug development. Parasite resistance to drugs and mosquito resistance to insecticides have led to a resurgence of malaria in many parts of the world, and there is a pressing need for vaccines and new drugs. AAA70078 to AAA70287 and AAB18144 to AAB18352 represent nucleotide and protein sequences given in the present invention, but which are not specifically mentioned within the
Tomato E-196 nucleotide sequence
                                 09-MAR-2001
                                                                   AAA95803;
                                                                                                   AAA95803 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2943 BP; 1587 A; 166
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                                                                                                                                                                                                                                                                                                                                      HisLeuThrAlaLysSerHisGlyArgValAsnAsn-----ValPheAspHisPheSer
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                                                                                                                                                                                                     LysLeuCysAspGlyIleAsnLysMetLeuAspGluGluAsn 187
                                                                                                                                                                                                                                                                                                                                                                          CAAGAACTTAAAAATATTATACAAGAATATGATGAAAGAATAGAAATTCAAAATAAGGAA 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnLeuAlaMetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnVal 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLys------LysLysValHis
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                                                                                                                                                                     AAGAAAAAAGAGGAAATAAATAAGCTCGTGGAAGAAAAAAGT 2100
                                                                                                                                                                                                                                                                        AspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPheLysProHisLeuGln
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Best Local Similari
                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes E-196, a polypeptide fragment isolated from CC the tomato. E-196 is a subfragment of the matrix attachment region (MAR) binding filament-like protein 1 (MFPI). A recombinant fusion protein CC comprising an N-terminal 6-histidine tag fused to E-196 was used to raise rabbit polyplonal antibody a288 against E-196. This was used to detect proteins with antigenic similarity to MFPI in other plant species. MFPI CC has features of a novel anchor protein that most likely connects chromatin via MAR DNA with the nuclear envelope and nuclear filament CC conference of the mechanisms underlying this process so that the attachment CC conference to the nuclear matrix may be used routinely to improve gene expression. They may be used to study MFPI expression, leading to the CC creation of novel development. In addition, if the reduction in expression of one of the genes leads to a growth or developmental defect in the
                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                 Sequence 588
                                                                                                                                                                                                                                                                                                                                                               plant, this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid fragments from tobacco, corn, soybean proteins that are homologs to the MAR binding filam (MFPI), useful for development of novel phenotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harder PA,
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 CAGGATCAGCTGAATTTGACTTCAGAGATCAAAGAACTTAAAGATGAAATCCAGAAA
                         LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                          TCTAAACTAGCTGAAAAAGAATCGGAGGTAAATAGTTTGAGCGATATGTATCAACAATCC 163
                                                                                      GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                 MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                                                                     TTGCTTACTACAGAGATCAAAGATAAAGAGGTGAGTCTTCGGAGTAAC-----ACC 103
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                                                                                                                                                                                                                                                                                                                                 BP; 223 A;
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MAR; NtMFP1-2; anchor protein;
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61 LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln 80 ::::::::::::::::::::::::::::::::::::
268 268 98 328 118 379 136 439 156 475 176 535

Search completed: July 28, 2005, 19:22:51 Job time : 563 secs

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-Q-/og/cgn2 1/USPTO_spool h/US10627571/runat 27072005 154722 27521/app_query.fasta_1.327
-Q-/ogn2 1/USPTO_spool h/US10627571/runat 27072005 154722 27521/app_query.fasta_1.327
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -STRATE1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HBAPSIZE=500 -MINLEN=0
-MAXIEN=200000000 -USER=US10627571 @CGN 1 1 480 @runat 27072005 154722 27521
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -MAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Copyright (c) 1993 - 2005 Compugen Ltd.
the number of results predicted by chance to have a
                                                      /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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APPLICANT: Zhao, Haoran
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 02104-00139US
CURRENT APPLICATION NUMBER: US/10/491,545A
CURRENT FILING DATE: 2004-04-01
PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID MOS: 96
SOPTWARE: PATENTIN Ver. 2.1
SEQ ID MO 48
LENGTH: 1892
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US-10-491-545A-48
          Score:
                            Alignment Scores: Pred. No.:
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APPLICANT: Li, Congfen
APPLICANT: Liao, X. Char
APPLICANT: Masuda, Esteb
APPLICANT: Pardo, Jorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 48, Application US/10491545A Publication No. US20050130117A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human TNF-induced protein GG2-1 mRNA,
OTHER INFORMATION: complete CDS
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17 US-10-616-1187-46
18 US-10-671-242-46
20 US-10-473-974-165
20 US-10-276-774-784
18 US-10-620-055-17
18 US-10-023-523-17
21 US-10-023-523-17
21 US-10-023-523-17
21 US-10-616-187-17
21 US-10-616-187-17
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22 US-10-671-242-17
23 US-09-938-842A-1473
24 US-09-938-842A-1473
25 US-09-938-842A-1473
26 US-09-938-842A-1473
27 US-09-981-752A-147
28 US-09-981-752A-147
29 US-10-872-768-2
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8 US-10-671-242-14

9 US-10-437-963-64679

9 US-10-437-953-53

7 US-10-425-112A-18136

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10S-10-425-115-178606

10S-09-792-630-40

10S-10-082-671-40

10S-10-082-671-40

10S-10-082-671-46
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      Length:
Matches:
      1892
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Sequence 46, Appl
Sequence 1784, Appl
Sequence 1784, Appl
Sequence 17, Appl
Sequence 1473, Ap
Sequence 1473, Ap
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 210, Appl
Sequence 14, Appl
Sequence 153, Ap
Sequence 53, Appl
Sequence 53, Appl
Sequence 53, Appl
Sequence 178606,
Sequence 40, Appl
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Query Match:
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US-10-627-571-1
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                                                                                                  APPLICANT: KASID, Usha N.
APPLICANT: KUMAR, Deepak
APPLICANT: KUMAR, Deepak
APPLICANT: GOKHALE, Prafulla
APPLICANT: GOKHALE, Prafulla
APPLICANT: HAMAD, Imran
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 223316
CURRENT APPLICATION NUMBER: US/10/627,571
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR APPLICATION NUMBER: US 60/264,062
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR APPLICATION NUMBER: PCT/US02/02212
PRIOR FILING DATE: 2001-01-28
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.2
SEQ ID NO 10-1
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10627571 Publication No. US20040082771A1 GENERAL INFORMATION:
                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
NAME/KEY: misc_feature
                                                                                       LENGTH: 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGACCGTGGTCAGTTTCCATCAGGTTGGATTATACCTTTTGACCGGAATGTGTTATCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
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FILE REFERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 215
LENGTH: 1814
TYPE: DNA
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Best Local Similarity:
Query Match:
DB:
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US-10-755-889-215
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                                                                                                                                                                                     Sequence 215, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED
TITLE OF INVENTION: PATHWAY
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             Sequence 217, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITITLE OF INVENTION: POLYNUCLEOTIDES AND POLY
ITITLE OF INVENTION: PATHWAY
FILE REFERENCE: DO284 NP
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 217
LENGTH: 2003
TYBE: NAME
PRIOR APPLICATION VERSION 3.2
LENGTH: 2003
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US-10-755-889-215
      TYPE: DNA
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APPLICANT: MOTTIS, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND M
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 497
LENGTH: 2034
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US-10-67-192-497
; Sequence 497, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOPTWARE: PATENTIN VERSION 3.2
SEQ ID NO 39
LENGTH: 2081
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US-10-087-192-497
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                                                                                                                                                                   Sequence 39, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES AND

TITLE OF INVENTION: PATHWAY

FILE REFERENCE: D0284 NP
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RESULT 7
US-10-087-192-496
US-10-087-192-496
; Sequence 496, Applicat
; Publication No. US2000;
; GENERAL INFORMATION:
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND M
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 496
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Best Local Similarity:
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ORGANISM: Homo
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; Sequence 98, Applicat
; Publication No. US200
; GENERAL INFORMATION:
; APPLICANT: Moore, Par
TITLE OF INVENTION: 110 Human Secreted Prote FILE REFERENCE: PZ021P1

CURRENT APPLICATION NUMBER: US/10/097,065

CURRENT FILING DATE: 2002-03-14

PRIOR APPLICATION NUMBER: PCT/US98/27059

PRIOR FILING DATE: 1998-12-17

PRIOR FILING DATE: 1997-12-18

PRIOR FILING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR FILING DATE: 1997-12-18

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Proteins

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; LENGTH: 58723
; TYPE: DNA
; ORGANISM: Homo s
US-10-087-192-496
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Best Local Similarity:
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AAAATGTTGGATGAAGAGAACATA
                                      LysMetLeuAspGluGluAsnIle 188
                                                                                                                     LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                                                                              TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
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APPLICATION NUMBER:

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Query Match:
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OTHER INFORMATION: r
NAME/KEY: SITE
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SOFTWARE: Patentin Var
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OTHER INFORMATION: n e NAME/KEY: SITE
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NAME/KEY: SITE
LOCATION: (161)
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APPLICATION NUMBER: 60/068,367
FILING DATE: 1997-12-19
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APPLICATION NUMBER: 60/068,054
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FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/068,369
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PRIOR FILING DATE: 1999-06-17
PRIOR PELICATION NUMBER: PCT/US98/27059
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR APPLICATION NUMBER: 60/070,923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,007
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
PRIOR FILING DATE: 1997-12-18
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PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,367
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068,368
PRIOR APPLICATION NUMBER: 60/068,369
PRIOR APPLICATION NUMBER: 60/068,169
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 98, Application US/103 Publication No. US20030204071A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 98
                                                                                                                                                                                                                                                                                                                                                                                                     Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: 110 Human Secreted Proteins FILE REFERENCE: PZ021P1
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/372,876
CURRENT FILING DATE: 2003-02-26
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                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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LOCATION: (1928)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                    NAME/KEY: SITE
LOCATION: (1934)
                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (1926)
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NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 494
LENGTH: 2087
TYPE: DNA
ORGANISM: Mus musculus
US-10-087-192-494
                                                                                                        GENERAL INFORMATION:

APPLICANT: MOXIG: David W.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVEL COMPOSITIONS AND N
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION UNMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
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US-10-087-192-494
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Best Local Similarity:
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Publication No. US20020182586A1
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APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US/9/747,377
PRIOR APPLICATION NUMBER: US/9/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-02
PRIOR FILING DATE: 2001-03-02
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Best Local Similarity:
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                           NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 493
LENGTH: 62231
                                                                                                                                                                                                                                                           GENERAL INFORMATION:
ORGANISM: Mus musculus
                TYPE: DNA
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Sequence 22314, Application US/10029386

Publication No. US20030194704A1

GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HARVENTION: EXPRESSION ANALYSIS TWO
FILE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
CURRENT APPLICATION UNUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 22914
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US-10-029-386-25411

Sequence 25411, Application US/10029386; Publication No. US20030194704A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David K.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SIN

TITLE OF INVENTION EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20
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NN: EXPRESSED IN HELA, SIGNAL = 2.3

NN: EXPRESSED IN HEALN, SIGNAL = 1.8

NN: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

NN: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

NN: EXPRESSED IN HEART, SIGNAL = 2.6
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FEATURE:

OTHER INFORMATION: MAP TO AC012678.1

OTHER INFORMATION: EXPRESSED IN HELLA, SIGNAL = 0.51

OTHER INFORMATION: SWISSPROT HIT: 061768, EVALUE 1.10e-01

OTHER INFORMATION: NT HIT: AF120995.1, EVALUE 1.30e-01

OTHER INFORMATION: EST_HUMAN HIT: BF744133.1, EVALUE 2.00e-59

US-10-029-386-25411
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                                                                                                                  Sequence 43, Application US/10094466 Publication No. US20030203363A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 25411
LENGTH: 527
                                           APPLICANT: Spytck et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
TITLE OF INVENTION: AND METHODS OF USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-290D
CURRENT APPLICATION NUMBER: US/10/094,466
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,281
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ORGANISM: Homo
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SEQ ID NO 43
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TYPE: DNA,
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: CDS
LOCATION: (2)..(566)
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OR APPLICATION NUMBER: 60/335,302
OR FILING DATE: 2001-10-31
OR APPLICATION NUMBER: 60/275,601
OR FILING DATE: 2001-03-13
OR APPLICATION NUMBER: 60/276,000
OR APPLICATION NUMBER: 60/276,000
OR FILING DATE: 2001-03-14
OR APPLICATION NUMBER: 60/277,338
OR FILING DATE: 2001-03-20
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FILING DATE: 2001-12-04
APPLICATION NUMBER: 60/275,579
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APPLICATION NUMBER: 60/275,
FILING DATE: 2001-03-12
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APPLICATION NUMBER: 60/288,148
FILING DATE: 2001-05-02
APPLICATION NUMBER: 60/274,849
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                                                                                             LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
                                                                                                                                                 ThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeu
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RESULT 15
US-10-094-466-41
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Best Local Similarity:
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CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/288,148
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/275,235
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NUMBER OF SEQ ID NOS: 114
SOFTWARE: PAIN 2.1
SEQ ID NO 41
LENGTH: 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo :
FEATURE:
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PRIOR APPLICATION NUMBER: 60/275,601
PRIOR FILING DATE: 2001-03-13
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TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
TITLE OF INVENTION: AND METHODS OF USING
TITLE OF INVENTION: THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/276,000
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LOCATION: (26)..(584)
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FILING DATE: 2001-03-12
APPLICATION NUMBER: 60/338,375
FILING DATE: 2001-12-04
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APPLICATION NUMBER: 60/335,302
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Publication No. US200:
GENERAL INFORMATION:
APPLICANT: YUE, Henr.
APPLICANT: YAO, Mon.
APPLICANT: GANDHI, J.
APPLICANT: BAUGHN, I.
APPLICANT: SWARMAKAI
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CURRENT APPLICATION NUMBER: US/10/416,314
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/247,505
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: US 60/249,642
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: US 60/249,824
PRIOR PILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,824
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APPLICANT:
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APPLICANT: KAREHT, Stephanie K.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: PI-0287 USN
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TAL, Preeti C
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WARREN, Bridget A.
HONCHELL, Cynthia D.
LU, Dyung Aina M.
THANGAVELU, Kavitha
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ISON, Craig H.
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GIETZEN, Kimberly J.
BURFORD, Neil
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CHAWLA, Narinder K.
SANJANWALA, Madhusudan M.
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PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/254,305
PRIOR ETLING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: US 60/256,448
PRIOR FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 130
SOFTWARE: PERL PROGram
SEQ ID NO 70
SEQ ID NO 70
; Sequence 5, Application US/0; Patent No. US20020150898A1; GENERAL INFORMATION: APPLICANT: Tang, Y. Tom APPLICANT: Zhou, Ping
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                                                                                             RESULT 17
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TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: misc feat
OTHER INFORMATION:
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                                                                                                                           ATGCTGGACGAGGGCAGCCTC
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; ORGANISM: Homo s
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174).
US-09-816-828-5
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TITLE OF INVENTION: No. US20020150898Alel Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIP2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR APPLICATION NUMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
NUMBER: 09 SEQ ID NOS: 18
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    TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLys
                                                HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
                                                                                                        LeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSer
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                                                                                          CTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCC
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Wang, Jian-Rui
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Asundi, Vinod
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APPLICANT: Tan, Yejun
APPLICANT: Dai, Hongyue
APPLICANT: Dai, Hongyue
TITLE OF INVENTION: Methods For Determining Whether An
TITLE OF INVENTION: Possesses A Defined Biological Act
FILE REFERENCE: ROSA122057
CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR APPLICATION NUMBER: US 60/474,413
PRIOR FILING DATE: 2003-01-24
PRIOR PILLING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
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US-10-764-420-2116
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SEQ ID NO 2116
LENGTH: 1389
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APPLICANT: Lum, Pek Yee
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LOCATION: 80
OTHER INFORMATION: n = A,T,C
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                                                           CTCAGCTTCCACCAGGTAGACTTCACCTTTGACCGGCGTGTGCTGGCCACTGGGCTGCTG
                                                                                                                      AATGAGCTGGCCCAGCTGCAGCGGTTCCGGGGCCGCGTCCGCAACCTGGCCATGACAGCC
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GENERAL INFORMATION:

APPLICANT: Wong, Gordon G.

APPLICANT: Wong, Gordon G.

APPLICANT: Fechtel, Kim

APPLICANT: Fechtel, Kim

APPLICANT: Agostino, Michael J.

APPLICANT: Howes, Steven H.

APPLICANT: Generick, Richard J.

APPLICANT: Gulukota, Kamalakar

APPLICANT: Graham, James R.

APPLICANT: GRAHAM J.

APPLICAN
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US-.09-822-849A-81
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PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys
                                                                                                                                                                                                         ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
                                                                                                                                                                                                                                                   IleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
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                                                                                          ĊTĠĠĊĊĊTĠĠĊTACCCĠĊTTTCĠĊĊAĠAĠĊTĠĊĠĠĠĠĠĠĠĊĠĊĠĠĠĊAĊŦŢĀĠĊ
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; NAME/KEY: CDS
; LOCATION: (100)..(651)
; FEATURE;
; PAME/KEY: sig_peptide
; LOCATION: (100)..(180)
US-10-363-374-15
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; Publication No. US20050048483A1
; GENERAL INFORMATION:
APPLICANT: Su, Eric
APPLICANT: Wang, He
: TITLE OF INVENTION: NOVEL SECRETED PROTEINS ANI
FILE REFERENCE: X13020
CURRENT APPLICATION NUMBER: US/10/363,374
; CURRENT FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 15
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US-10-363-374-15
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ORGANISM: Homo
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                          PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys 125
                                                                                         LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
                                                                                                                          ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
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                                                                                                                                                                                        CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCAGCGCGTGATCAAGGACCTG
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CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGGGTGCCATGACGGCACTTAGC
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APPLICANT: Tang, Y: Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NO. US20040053250Alel Arginine-rich Pro
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803_1CNCP
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR APPLICATION NUMBER: US 09/799,451
PRIOR APPLICATION NUMBER: US 09/799,451
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SEQ ID NO 537
LENGTH: 1175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
NAME/KEY: CDS
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ORGANISM: Homo
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                                                                                                                                                                                             242
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                                                                                                                                     66 IleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                                                                                                                                                                                     46 ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                                                                                                                                                                                            26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
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PheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArgLeuLeuAsnGluCys
                                                                                                                 ATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATGGCTCCTTTGGCCCCAGTGAG
                                        CTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCCGCAGGGTGCCATGACGGCACTTAGC
                                                                            LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer
                                                                                                                                                                                           CGTGTGTCCAAGGAGTACACGCACAGCCGGGCCCCAGGCGCGCGTGATCAAGGACCTG
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5. US20040053250A1
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Conservative:
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Best Local Similarity:
Query Match:
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US-10-959-539-59
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/959,539
CURRENT FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US/10/031,915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: SHAH, Purvi
TITLE OF INVENTION: CELL CYCLE AND PROLIFERATION PROTEINS
FILE REFERENCE: PF-0722 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                         172 CGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
                                                                                                                                                 112 TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGGAAGAAGCTACTGAGTAAGATGGCGGGT
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                                      46
                                                                                                       26 LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
                                                                                                                                                                           6 PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer
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                                 ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
CGTGTGTCCAAGGAGTACACGCACAGCCGGCCCAGCGCCCAGCGCGTGATCAAGGACCTG
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LU, Dyung Aina M.
BAUGHN, Mariah R.
PATTERSON, Chandra
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BANDMAN, Olga
AZIMZAI, Yalda
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YUE, Henry
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/10959539
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Matches:
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US-09-796-692-3207
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                 Alignment Scores: Pred. No.:
                                                                           US-09-796-692-3207
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
                                                                                                                                                 SOFTWARE: FastSEQ
SEQ ID NO 3207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
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                                                                                                                                                                                    PRIOR FILING DATE: 2000-08
NUMBER OF SEQ ID NOS: 9597
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CURRENT APPLICATION NUMBER: US/99/796,692
                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
                                                                                           ORGANISM:
                                                                                                              TYPE:
                                                                                                                              LENGTH: 287
                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/223,416
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/222,903 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/218,950
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/206,201
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2.01e-47
504.00
Length:
Matches:
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/440,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
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Best Local Similarity:
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US-10-040-862-3207
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                         SOFTWARE: Fast
SEQ ID NO 3207
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
                                                                                                                          PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
                                                                                                            NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/223,416 FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-05-04
APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mannion, Jane
Retter, Marc
Corixa Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspArgAsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIle 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IleLeuTyrArgAsnAsnGlnPheAsnGlnAspGluLeuAlaLeuMetGluLysPheLys
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                                                                                Version 3.0
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Indels:
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                                                                  FILE REPERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-01
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
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Best Local Similarity:
Query Match:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compositions and Methods for the TITLE OF INVENTION: Hematological Malignancies
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                           APPLICATION NUMBER: US 60/222,903 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 AspArgAsnValLeuSerArgLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIle
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Prior Application data removed -
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Clapper, Jonathan
Wang, Aijun
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Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Matches:
Conservative:
Mismatches:
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See File Wrapper or PALM
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Therapy

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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Dete
TITLE OF INVENTION: Compositions and Methods for the Dete
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 0.4058-013521US
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-05-02
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
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US-10-154-884B-3207
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3207
LENGTH: 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3207, Application US/10154884B Publication No. US20040005561A1
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Indels:
Gaps:
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APPLICANT: COTICAL, Malical APPLICANT: COTICAL, Malignancies
FILE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
FITTLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US

CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR RILING DATE: 2001-11-06
PRIOR FILING DATE: 2001-11-06
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,79
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,799
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,099
PRIOR APPLICATION NUMBER: US 60/200,09
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NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Matches:
Conservative:
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CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PPLICATION NUMBER: 60/290,479
PRIOR PPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR PPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/208,201
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Best Local Similarity:
Query Match:
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; ORGANISM: Homo sapiens
US-10-764-324-3207
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-07-14
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FILING DATE: 2000-07-14
APPLICATION NUMBER: 60/
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RESULT 29
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Best Local Similarity:
Query Match:
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                                                                                                                         GENERAL INFORMATION:
                                                                                                                                          Sequence 2801, Application US/10040862 Publication No. US20030078396A1
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                APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
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PRIOR FILING DATE: 2000-08-04
PRIOR PPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
NUMBER OF SEG ID NOS: 9597
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Sequence 2801, Application US/10040862

Sequence 2801, Application US/10040862

Publication No. US20030078396A1

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Mannion, Jane

APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis

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APPLICANT: Wang, Ajun

APPLICANT: Ordonez, Nadia

APPLICANT: Carter, Lauren

APPLICANT: McNeill, Patricia Dianne

TITLE OF INVENTION: Compositions and Methods for the Detection, Diannel

TITLE OF INVENTION: Hematological Malignancies

FILE REFERENCE: 014058-014402US

CURRENT APPLICATION NUMBER: US/10/057,475B

CURRENT FILING DATE: 2000-03-01

PRIOR APPLICATION NUMBER: US 60/186,126

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR APPLICATION NUMBER: US 60/190,479

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR APPLICATION NUMBER: US 60/200,545

PRIOR FILING DATE: 2000-04-27
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan
APPLICANT: Wang, Aijun
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PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR PILING DATE: 2000-08-07
PRIOR PILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
PRIOR FILING DATE: 2001-03-01
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LENGTH: 287
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SOFTWARE: FastSEQ for Windows Version
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ORGANISM: Homo
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Clapper, Jonathan David
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US-10-154-884B-2801/c
Sequence 2801, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
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Best Local Similari
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PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
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LENGTH: 287
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                 CURRENT APPLICATION NUMBER: US/10/154,884B CURRENT FILING DATE: 2002-05-23 PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: US 60/190,479 PRIOR FILING DATE: 2000-03-17
                                                                                                                                                               TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013521US
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FILLING DATE: 2000-04-28
RAPPLICATION NUMBER: US 60/200,779
FILLING DATE: 2000-04-28
RAPPLICATION NUMBER: US 60/200,999
FILLING DATE: 2000-05-01
APPLICATION NUMBER: US 60/200,545
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Methods, Marc
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagonal Experimental Compositions and Methods for the Detection, Diagonal Composition of Compositions and Methods for the Detection, Diagonal Composition of Compositions and Methods for the Detection, Diagonal Composition and Detection and De
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NUMBER OF SEQ ID NOS: 11290
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2801
LENGTH: 287
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ORGANISM: Homo sapiens
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OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,999
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: US 60/202,084
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: US 60/206,201
OR APPLICATION NUMBER: US 60/206,201
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
           APPLICATION NUMBER: US 60/186,126 FILING DATE: 2000-03-01
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FILING DATE: 2000-04-28
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THI
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
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                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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Percent Similarity:
Best Local Similarity:
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LENGTH: 287
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SOFTWARE: PastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
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APPLICATION NUMBER: US 60/206,201
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APPLICATION NUMBER: US 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
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FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,779
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                           154 AspCysGluPheLeuAlaAlaLeuTyrAsnProPheGlyAsnPhe 168
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GATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTT
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APPLICATION NUMBER: 60/200,303 FILING DATE: 2000-04-28 APPLICATION NUMBER: 60/200,779

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DATE:

2000-04-27

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NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n
NAME/KEY: unsure
LOCATION: (59)
OTHER INFORMATION: n
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Query Match:
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                                                                                                                US-10-040-862-5724
                                                                                                                                   RESULT
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SOFTWARE: FastSEQ for Windows Version SEQ ID NO 5724
Sequence 5724, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
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ORGANISM: Homo
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PR APPLICATION NUMBER: 60/200,999

PR FILING DATE: 2000-05-01

PR APPLICATION NUMBER: 60/202,084

PR FILING DATE: 2000-05-04

PR FILING DATE: 2000-05-04

PR APPLICATION NUMBER: 60/206,201

PR APPLICATION NUMBER: 60/218,950

PR FILING DATE: 2000-07-14
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FILING DATE: 2000-08-03
APPLICATION NUMBER: 60/223,416
FILING DATE: 2000-08-04
APPLICATION NUMBER: 60/223,378
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APPLICANT: Corixa Corporation
ITITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
ITITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 0.14058-013520US
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
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Query Match:
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LENGTH: 288
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NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: r
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PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR FILING DATE: 2000-08-03
PRIOR PPLICATION NUMBER: US 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: US 60/223,378
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
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SOFTWARE: FastSEQ
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NAME/KEY: unsure
LOCATION: (59)
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                      eGlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsnValPheAspHisPheSe
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NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5724
LENGTH: 288
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PRIOR FILING DATE: 2000-03-01
PRIOR PPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
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CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
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Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Clapper, Jonathan David
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US-10-627-571-2 (1-188) x US-10-154-884B-5724 (1-288)
                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR RFILING DATE: 2000-03-01
PRIOR RFILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                   US-10-154-884B-5724
                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 11290
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 5724
LENGTH: 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap TITLE OF INVENTION: Hematological Malignancies
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                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (1)...(288)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                    No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-044-28
APPLICATION NUMBER: US 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/218,950 FILING DATE: 2000-07-14 APPLICATION NUMBER: US 60/222,903 FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/206,201 FILING DATE: 2000-05-22
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Retter, Marc W.
Corixa Corporation
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Alignment Scores:
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US-10-764-324-5724
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PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR PILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
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                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ
SEQ ID NO 5724
LENGTH: 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
LOCATION: (58)
                                                                                                                                                                                                                                                                                                                            Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2001-11-06
                                                                                     LOCATION: (59)
OTHER INFORMATION:
                                                                                                                           FEATURE:
NAME/KEY: unsure
                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/218,950 FILING DATE: 2000-07-14
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; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION UNMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
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US-09-918-995-35521
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Best Local Similarity:
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US-09-918-995-35521
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 35521
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TYPE: DNA
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IleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPheAsnGlnAspGlu
                                                              CGTGTGTCCAAGGAGTACACGCACAGCCCGGCCCAGGCCCAGCGCGTGATCAAGGACCTG
                                                                                                                                                                     LysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeuAspGluLeuTyr
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                                                                                                                                                                                                                     TTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAAGAAGCTACTGAGTAAGATGGCGGGT 136
                                                                                       ArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLysIleLysAsnLeu
                                                                                                                                              CGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTGAGGTGCTAGATGAGCTCTAC
                                                                                                                                                                                                                                            PheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGlyLysMetValSer 25
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97.92%
97.92%
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Matches:
Conservative:
Mismatches:
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OTHER INFORMATION: E OTHER INFORMATION: N OTHER INF
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US-10-972-079-232
Sequence 232, Application US/10972079
Publication No. US20050153317A1
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Best Local Similarity:
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US-10-029-386-9211
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 9211
LENGTH: 500
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                            GENERAL INFORMATION
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                         APPLICANT:
                                                                                                                                                        APPLICANT: MMI GENOMICS, INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
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                                                                                                                                                                                                                                                                                                                                                                           AAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                LysLeuCysAspGlyIleAsnLysMetLeuAspGluGluAsnIle 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GATTGTGÄATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuAlaLeuMetGluLysPheLysLysLysValHisGlnLeuAlaMetThrValValSer 105
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                                                                                         DeNISE, Sue K.
ROSENFELD, David
                          KERR, Richard
BATES, Stephen
HOLM,
Tom
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N: EXPRESSED IN HELA, SIGNAL = 2.3

N: EXPRESSED IN BRAIN, SIGNAL = 1.8

N: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

N: EXPRESSED IN HEART, SIGNAL = 2.4

N: NT HIT: 9114725421, EVALUE 0.00e+00

N: EST_HUMAN HIT: BG178783.1, EVALUE 0.00e+00
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US-10-191-803-330/c
                                                        Alignment Scores:
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Best Local Similarity:
Query Match:
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; TYPE: DNA
; ORGANISM: Chicken
US-10-972-079-232
                             Pred. No.:
                                                                                                                          US-10-191-803-330
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SEQ ID NO 232
                                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                                                                                                                    TYPE: DNA
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APPLICANT: JOHNSON, Kory
APPLICANT: JOHNSON, Kory
APPLICANT: CASTLE, Arthur
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/377,611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michae
                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. SEQ ID NO 330
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Publication No. US20040014040A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/972,079
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: US 60/514,333
PRIOR FILING DATE: 2003-10-24
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                                                                                                                                                                                   ORGANISM: Rattus norvegicus FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              529 CTGTACAAGGTGACAAAGGAACACCACAGAAACAAA 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                469 GCAACCAAAACCATGGCTAACATGCTCATCGATGACACGAGCAAGCGAAATCTTTGATGAG
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DB:
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Best Local Similarity:
                                                                                                                                           US-09-796-692-4917/c
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                                                                               Sequence 4917, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 11708
LENGTH: 543
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: ABOMICA-X-2
                APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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OTHER INFORMATION: MAP TO ACO12678.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.51
OTHER INFORMATION: EST HUMAN HIT: BG107777.1, EVALUE 0.00e+00
OTHER INFORMATION: NT HIT: AB002705.1, EVALUE 5.20e-01
OTHER INFORMATION: SWISSPROT HIT: P45815, EVALUE 3.90e+00
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                                                                                                                                                                                                                          183 LeuAspGluGlu 186
                                                                                                                                                                                                                                                                                                        163 AsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLysMet 182
                                                                                                                                                                                                                                                                                                                                                                                     143 GlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeuTyr
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Det
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/180,479
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-17
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Best Local Similarity:
Query Match:
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; NAME/KEY: unsure
; LOCATION: (77)
; OTHER INFORMATION: n=A,T,C
US-09-796-692-4917
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CURRENT PILIUG DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR PELICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
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; LENGTH: 538
; TYPE: DNA
                                                                                                                                                                                                                                                                                                                                        Sequence 4917, Application US/10040862 Publication No. US20030078396A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/223,416
PRIOR ETLING DATE: 2000-08-03
PRIOR ETLING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
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SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
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PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
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PRIOR APPLICATION NUMBER: 60/200,999
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Matches:
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Therapy

APPLICATION NUMBER: US 60/200,303 FILING DATE: 2000-04-28

APPLICATION NUMBER: US 60/200,545 FILING DATE: 2000-04-27

FILING DATE: 2000-04-28

APPLICATION NUMBER: US 60/200,779

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RESULT 45

US-10-057-475B-4917/c

¡ Sequence 4917, Application US/10057475B

¡ Publication No. US20040002068A1

¡ GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

¡ APPLICANT: Mannion, Jane

¡ APPLICANT: Mannion, Jane

¡ APPLICANT: Clapper, Jonathan David

APPLICANT: Mang, Aijan
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Best Local Similarity:
Query Match:
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US-10-040-862-4917
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4917
APPLICANT: Corian Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
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APPLICATION NUMBER: US 60/223,378
FILING DATE: 2000-08-07
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APPLICATION NUMBER: US 60/223,416
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APPLICATION NUMBER: US 60/218,950
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APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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                                                                                                                                                                                                            Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Percent Similarity:
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Query Match:
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Search completed: July 28, 2005, 19:36:11 Job time : 671 secs
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                                                                                                                                                                                                                                                            Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/218,950 PRIOR FILING DATE: 2000-07-14 PRIOR APPLICATION NUMBER: US 60/222,903 PRIOR FILING DATE: 2000-08-03 Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 10979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR
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LOCATION: (1)...(538)
OTHER INFORMATION: n =
                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 538
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
                                                                   538 AAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGA
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Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool h/US10627571/runat_27072005 154720 27509/app_query.fasta_1.327
-Q=/cgn2 1/USPTO_spool h/US10627571/runat_27072005 154720 27509/app_query.fasta_1.327
-DB=EST -QFMT=fastap -SUFPIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10627571 @CGN 1 1 3437 @runat 27072005 158720 27509 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQÜERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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No.
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Listing first 100 summaries
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Perfect score:
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                                                                                                                                                                                        Score
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length: 2000000000
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Fgapop 6.0 , F
Delop 6.0 , F
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962
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Contact: Brandenberger R
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from DMSO-treated hBS cell line H9 (p22) maintained in
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                                                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM389 row: j column: 24 High quality sequence stop: 635.
                                                                                                                               and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. J
                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                              Mammalia; Eutheria; Primates; Catarrhini; 1 (bases 1 to 780)
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             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30347855"
/tissue_type="Human Placenta"
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sapiens cDNA clone
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Collection

(MGC)

Euteleostomi;

Homo

EST 01-MAY-2003

180

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646

(NHGRI)

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IMAGE:30528465 5', mRNA sequence
CF593784
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sapiens (human)
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/note="Organ: placenta; Vector: pBluescriptR; Site 1:
all-XhoI; Site 2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
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Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 2089
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High quality sequence stop: 648.
Location/Qualifiers
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National Institutes of Health, N
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                  PheAsnGlnAspGluLeuAlaLeuMetGluLysPheLysLysValHisGlnLeuAla
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(bases 1 to 806)
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//clone_lib="NIH_MGC 147"
//clone_logan: placenta; Vector: pBluescriptR; Site 1:
//note="Organ: placenta; Vector: pBluescriptR; Site 1:
//note="Organ: placenta; Vector: primed using primer
//note="Organ: placenta; Vector: primed using primer
//note: Site 2: BamH; Oligo-dT primed using primer
//normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
a NIH_MGC library."
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/lab_host="DH10B TonA"
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/clone="IMAGE:30528465"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian
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AGENCOURT 15178772 NIH MGC 192 Homo sapiens
IMAGE:30512832 5', mRNA sequence.
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                                                                                                                                                                                                                  Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 2089
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National Institutes of Health, M
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                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
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                       SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
                                                                                                                                                             ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTTGACCGGAATGTGTTATCCAGG
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TCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC
                                                                           CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
                                                                                                      LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys 140
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/tissue_type="Brain glioblastoma"
/tissue_type="Brain glioblastoma"
/lab_host="DH108 (T1 phage-resistant)"
/clone_lib="MIH_MGC 192"
/note="Vector: pExpress1; Site_1: Smal; Site_2: Not1; The
library was constructed by reverse transcription of 1 ug
mRNA using the oligo dT primer GCGGCCGCCC(T)20 and an
RNaseH + MMLV reverse transcriptase. Second strand
synthesis was carried out by standard methods. The cDNA
was size selected by agarose gel for > 1.2 kb, digested
with Not I and directionally cloned into the vector
Express-1 at the Smal/NotI sites. DNA from the primary
library was used for in vitro transcription from the T'
promoter to produce biotinylated RNA transcripts. These
biotinylated transcripts, along with blocking oligos to
the poly-A, multiple cloning site and primer regions, were
hybridized with single stranded circles produced by
phagmeid production from the primary library to a Cot
value of 10-20. Strepavidin/phenol extraction was utilized
stranded circles which were repaired by primer extension
and transformed back into E. coli resulting in the
normalized library. Average insert size 2.0 kb. 3'
linker/adaptor sequence GCGGCCCCC(T)20. This libary was
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Best Local Similarity:
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                                                                                        41 LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                  21 GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J and Stanton, L.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Regenerative Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: rbrandenberger@geron.com
Insert Length: 712 Std Error: 0.00
Location/Qualifiers
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Fax: 650 473 7760
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                   LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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                                                                   CTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="GRN_ES"
/note="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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AGENCOURT 14353034 NIH MGC 191 Homo
IMAGE:30413002 5', mRNA sequence.
CD521721
CD521721.1 GI:31453439
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                         Plate: NDCM207 row: e column: 11
High quality sequence stop: 603.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Narayan Bhat CDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
.national Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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/clone="IMAGE:30413002"
/tissue_type="Pooled"
/tissue_type="Pooled"
/lab_host="ph10B (T1 phage-resistant)"
/clone_lib="NIH MGC 191"
/clone_lib="NIH MGC 191"
/note="Vector: phNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood
Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts
                                                                                                                                                                                                                                           organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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o sapiens cDNA clone
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US-10-627-571-2 (1-188) x CD521721 (1-731)
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteléostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1055)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                              AGENCOURT 6715690 NIH MGC_120 5', mRNA sequence.
BM919223
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plate: LLMM12776 row: d column: 11
High quality sequence stop: 677.
Location/Qualifiers
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/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EccRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(BcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
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/clone="IMAGE:5788442"
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Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

let strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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On Feb 15, 2001 this sequence version replaced gi:31271310.
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| TleLygAsmLeuIleLygTmrValIleLygLeuAlaIleLeuTyrArgAsmAsmGlnPhe
                                                                                  GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAGAGAAGATC
                                                                                                             AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
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/clone_lib="tomo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist "trand cDNA was primed with a NotI-oligo(dT).
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI044YG13"
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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On Feb 15, 2001 this sequence version replaced gi:31272274
Contact: Genoscope
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                               Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr Neb: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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more information about this cluster, see
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full-length cDNA clone Cof Homo sapiens (human). CR611795 CR611795, I GI:50492602 HTC; CNSLT_cDNA.
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Liwas normalized. Library was constructed by Life Technologies, division of Invitrogen.
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http://fulllength.invitrogen.com/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="CSODIO57YA07"
/tissue_type="Placenta Cot 2
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vitrogen.com/ InVitroGen Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JUL-2004) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
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CR615621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                           AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys
                                                                                                                             AAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACAAAGTAGTGAGGTGCTG
                                                                                                                                                 LysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluValLeu
                                                                                                                                                                                                   GCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGT
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Neuroblastoma Cot 25-normalized"
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Submitted (20-UUL-2004) Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genosco-
Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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/plasmid="pCMVSPORT_6"
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                                      CDNA Library Preparation: Life Technologies, Inc. (CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM13492 row: f column: 02 High quality sequence stop: 596.
                                                                                                                                                                  Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 996)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Macaca mulatta
                                                                     998 bp mRNA linear EST 13-MAY-2004 ILLUMIGEN MCQ_30108 Katze_MMPB Macaca mulatta cDNA clone IBIUW:8795 5' similar to Bases 72 to 998 highly similar to human TNFAIP8 (Hs.17839), mRNA sequence.
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
Technologies."
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
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/clone="IMAGE:6153217"
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Plate: CL000256 row
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Sequenced on 2004.03.27. 798 (
PCR PRimers
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Illumigen Biosciences.Inc.
2203 Airport Way S, Suite 450,
Tel: 2063780400
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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ATGACCGTGGTCAGTTTCCACCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
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/note="Vector: Uni_ZAP XR; Site 1: EcoR I; Site 2: Xho I;
Created from Stratagene ZAP-cDNA Synthesis kit (Catalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit (Catalog #200450)"
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/clone="IBIUW:6795"
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/mol_type="mRNA"
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/strain="Indian"
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1 (bases 1 to 1045)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31275981.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                       N
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was dispetted with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Fobo,G., Han,M. and W
Pongo pygmaeus mRNA (
Unpublished (2004)
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                                                                                 Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiema Molecular Genome Analysis, German Cancer Research Center (DKFZ) Email s. wieman@dkfz-heidelberg.de, sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZ)692132) is available the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdma/.
                                                                                                                                                                                                                                                                                                          Contact: MIPS
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Mammalia; Eutheria; Primates;
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Pongo pygmaeus
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/db_xref="taxon:9600"
/clone="DKFZp469E1232"
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5', mRNA sequence
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BI752550.1 GI:
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               Homo sapiens (human)
Homo sapiens (buman)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 876)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec
                                                                                                                                                                                                603021969F1 NIH_MGC_114
Unpublished (1999)
                                                                                                                                                                                                                                                                                                        AAAATGTTGGATGAAGAGAACATA
                                                                                                                                                                                                                                                                                                                                                          TTGTATAATCCTTTTGGGAATTTTTAACCCCACTTACAAAAACTATGTGATGGTATCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="kidney"
/dev stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.92e-102
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Best Local Similarity:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1481 row: j column: 18
High quality sequence stop: 813.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                                                                               LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACACACAGTAGTGAGGTG
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LeuTyrAsnPro-PheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAs 180
                                                         SerHisGlyArgValAsnAgnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
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                                                                                                                                                                               ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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BP433798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: huenishi@affrc.go.jp

BST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Animal Genome Laboratory, Genome Research Department National Institute of Agrobiological Sciences 2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan Tel: +81-29-838-8627 Fax: +81-29-838-8627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 773)
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EST.
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                                                                                        GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                        nLysMetLeuAspGluGluAsnIle 188
                   LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                   GTGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="LNG010079A10"
/tissue_type="lung"
/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                           clone_lib="full-length enriched swine cDNA library, adult
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JOURNAL COMMENT
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ORGANISM
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CN789950
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                                                                                                                                                                                                                                                                        Contact: Richard G. Baumann
Bovine Functional Genomics La
ANRI
BLDG 162: BARC-EAST, Beltsvil
Tel: 3015048604
Fax: 3015048744
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CN789950.1
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Baumann,R.G., Baldw
Matukumalli,L.K.
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Bos taurus
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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h quality sequence stop: 669.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                      162: BARC-EAST, Beltsville,
/tissue_type="Epithelial, Muscle"
/dev_stage="Lactating, Neonatal"
/lab_host="DH10B TONA"
/clone_lib="BARC 8BOV"
                                                       /db_xref="taxon:9913"
/clone="8BOV_35M20"
/sex="Female"
                                                                                                             organism="Bos taurus"
/mol_type="mRNA"
                                                                                              /strain="Holstein"
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AUTHORS
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/note="Organ: Intestine; Vector: pCMVSport6.1; Site 1: Not1; Site 2: EcoRI; Normalized cow cDNA intestinal library in pCMVsport6.1, constructed from equimolar mRNA pools derived from 5 sources, 4 lactating intestinal, 1 neonatal intestinal 4/5 Lactating, Proximal Duodenum, Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Distal Ileum, Colon, 1/5 Neonatal, Proximal Duodenum, Jejunum, Distal Ileum"

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US-10-627-571-2 (1-188) x CN789950
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AGENCOURT 11295099 NIH MGC 164 Mus
IMAGE: 30146475 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 942) NIH-MGC http://mgc.nci.nih.gov/.

Mus musculus

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Best Local Similarity:
Query Match:
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http://image.llnl.gov
plate: NDAM062 row: d column: 04
High quality sequence start: 21
High quality sequence stop: 693.
Location/Qualifiers
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Tissue Procurement: Dr. David Rowe and Dr. Mina
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Contact: Robert Strausberg,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                                   ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
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                                                                                            CTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAAG
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/(lab host="DH10B (phage-resistant)"
/(lab host="DH10B (phage-resistant)"
/(clone_lib="NIH_MGC_164"
/(clone_lib="NIH_MGC_164"
/(note="Vector: pCMV-SpORT6.1; Site_1: EcoRV; Site_2: NotI;
/(note="Vector: pCMV-SpORT6.1; Site_
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/db_xref="taxon:10090"
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AUTHORS
TITLE
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11457 row: k column: 04
High quality sequence start: 5
High quality sequence stop: 869.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 893)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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603042814F1 NIH_MGC_116
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//clone_lib="NIH_MGC_116"
//note="Organ: pooled colon, kidney, stomach; Vector:
//note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183355"
                                                                                                                      4.94e-101
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                              source
                                   Tel: +49 30 8413 101.

Fax: +49 30 8413 1380

Email: hennig@molgen.mpg.de

EST's are made from clones being representatives of clone clusters.

Clone clusters were calculated from oligonucleotide fingerprints.

PCR PRimers

FORWARD: 5'-GAGCTATTCCAGAAGTAGTGA-3'

BACKWARD: 5'-TAATACGACTCACTATAGGG-3'.

Seg primer: 5'-ATTAGGTGACCTATAGGG-3'.

Seg primer: 5'-ATTAGGTGACTGACTATAGGG-3'.
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                                                                                                                                                                                        Contact: Hennig S
Laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
                                                                                                                                                                                                                                                                               Yahyawi,M., Hennig,S., Neidhardt,L., Radelof,U., Hermann,B.G., Lehrach,H. and O'Brien,J.
Detection of a high number of novel genes in a 9-day mouse embryo CDNA library normalised by oligonucleotide fingerprinting Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF607236 832
MY1_00178 Mouse 9-day fetus
cDNA_clone ICRFp522C0838 5',
BF607236 BF607236.1 GI:13503728
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 832)
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                                                                                                                                                                                                                                                                                                                                                                                                        musculus
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organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
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696

719

Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

Mus

CA469176 841 bp AGENCOURT 10735591 NIH MGC 154 Mus IMAGE:30122433 5', mRNA sequence. CA469176 CA469176.1 GI:24925528

musculus mRNA

linear tinear EST

09-MAR-2004

Mus musculus

(house

mouse)

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US-10-627-571-2 (1-188)
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Best Local Similarity:
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LysMetLeuAspGluGluAsnIle 188
                                                                      LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                                    TCTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGATTGTGATTTTTTGGCTGCC
                                                                                                                                        SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                                                                            CTGCTGAACGAGTGCCGAGAGCTCCTACACGAGGATCATTCAGCGCCACCTTACCGCCAAG
                                                                                                                                                                                                               LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="ICRFp522C0838"
/tissue_type="whole embryo"
/dev_stage="embryonic 9-day"
/lab_host="E.coli, XII blue"
/clone_lib="Mouse 9-day fetus cDNA library ICRFp522"
/note="Vector: PSVSport1; Site 1: Not1; Site 2: Sal1;
Library preparation by oligo_dT priming of RNA. Clones be ordered from the Resource Center in Berlin, http://www.rzpd.de."
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bradfield Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                    MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
                                                                                                                                                                          GTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAG
                                                                                                                                                                                        LysIleLysAsnLeuIleLysThrVallleLysLeuAlaIleLeuTyrArgAsnAsnGln
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CTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAAG
             LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                        ATGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGG
                                                                       MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
                                                                                                                  TTCAATCAAGACGAGCTGGCGCTCATGGAGAAGTTCAAGAAGAAGGTGCACCAGCTTGCC
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/db_xref="taxon:10090"
/clone="IMAGE:30122433"
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Percent Similarity:
Best Local Similarity:
Query Match:

1.09e-100 920.00 98.94% 94.15% 95.63%

Conservative: Mismatches: Indels:

Length: Matches:

Score:

Pred.

No.:

US-10-627-571-2 (1-188) x BI525793 (1-865)

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RESULT 26
BI525793
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11155 row: o column: 13
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Tissue Procurement: Gilbert Smith,
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento
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                                                                                                                                                                                                                                                                                                                                                                       e: LLAM11155 row: o column: quality sequence start: 28 quality sequence stop: 829.
                                          Ph.D.
                                                                                                                                                                                                                                                                          /strain="CZECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                            clone="IMAGE:5057508"
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                                                                            Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY
Email: segrefogenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 559)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31283006.

Contact: Genoscope
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AL558873
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AL558873
AL558873.3 GI:46184260
                           For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODJ015DD02QP1&c=3485.f. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORWALIZED
iens cDNA clone CS0DJ015YH04 5-PRIME, mRNA sequence.
/organism="Homo sapiens"
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Best Local Similarity:
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ORGANISM
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BP302623 Sugano cDNA library, m

MPE06324, mRNA sequence.

BP302623
BP302623.1 GI:52231583

EST.
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sapiens
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                                                                              /mol_type="mRNA"
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/db xref="taxon:9606"
/clone="CSDDJ015YH04"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORWALIZED"
/cell_line="JURKAT"
/clone_lib="JURKAT"
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US-10-627-571-2 (1-188) x AL558873 (1-559)
TyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsnLys
                                                                             CATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCTTG
                                                                                                  HisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAlaLeu
                                                                                                                                                             TTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCA
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Matches:
Conservative:
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(human)

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Homo

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EST 17-SEP-2004

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AUTHORS
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1 (bases 1 to 580)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                            MetLeuHisGlnIleIleGlnArgHisLeuThrAlaLysSerHisGlyArgValAsnAsn
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                                          Ile 188
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Best Local Similarity:
Query Match:
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AUTHORS
TITLE
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Tissue Procurement: David Segal Ph.D., Herbert Morse M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:1478145
Seg primer: -40RP from Gibco
High quality sequence stop: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
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National Cancer Institute, Cancer Genome Anatomy
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 651)
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                        LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln 80
                                                                                            LeuAspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLys
                                                                                                                                                                           GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                                                                                                                                                                                                       MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
GTCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAG
                                                                                                                                                     GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACCACCAGCGAGGTG
                                                                                                                                                                                                                                 ATGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="NCI_CGAP_Sp2"
/note="Organ: spleen; Vector: pCMV-SPORT6 (Life
/note="Organ: spleen; Vector: pCMV-SPORT6 (Life
Technologies); mRNA made from flow-sorted NK cells, cDNA
made by oligo-dT priming. Directionally cloned. Average
insert size 1.5 kb. Primary library, non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db xref="taxon:10090"
/clone="IMAGE:3978113"
/clssue type="NK cells (flow-sorted)"
/lab_host="DH10B (Tl-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
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916.00
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94.15%
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                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
    US-10-627-571-2
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                                                                                                                                                                                                                                                                                                                                                                  Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chi
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          628
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AU135377
                                                                                                                                                                                                                                                                                       Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawa Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRI human cDNA
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1 (bases 1 to 816)
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                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1001920"
                                                                                                                                                                                                                                  organism="Homo
mol_type="mRNA'
                                                                                                                                                                           'tissue_type="placenta"
'clone_lib="PLACE1"
                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                             3.08e-100
916.00
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; Homo.
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                                                                                Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konmo, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
                                                                                                                                                                                                     Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
                                                                                                                                                                                                                                                                                                                                                                                               AK090316

1542 bp mRNA linear HTC 03-i
Mus musculus 14 days embryo lung cDNA, RIKEN full-length en
library, clone:G630049H02 product:TNF-INDUCED PROTEIN GG2-1
                                                                                                                                                                                                                                                                                          Eukaryota;
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HTC; CAP trapper.
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

L Nature 420, 563-573 (2002)

E 6 (bases 1 to 1542)

Radachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, T., Hayashida, K., Hayatsu, M., Hiraoko, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kotho, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. prepare wist our web site for further details. URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-Cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in R
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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homolog [Homo sapiens] (SPTR|Q9UP47, evidence: FASTY,
93.6%ID, 100%length, match=565)
                                                                /trānslation="mlseaeeprevatdvfnsknlavqaqkkilgkmvsksiattlid
dtssevldelyrvtkeytqnkkeaerviknliktviklavlhrnnqfnqdelalmekf
kkkvhqlamtvvsfhqveytfdrnvlsrllnecrellheiiqrhltakshgrvnnvfd
                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN fu
/dev_stage="14 days
118. ...714
                                              HFSDCDFLAALYNPFGKFKPHLQKLCDGIKKMLDEENI"
                                                                                                                                 /codon_start=1
/protein_id="BAC41167.1"
/db_xref="GI:26355503"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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Mammalia; Eutheria; Rodentia; Scii
1 (bases 1 to 908)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Man
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
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Procurement: Jeffrey Green
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Mismatches:
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                                           Ph.D
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Sciurognathi; Muridae;
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                                                                                       Gene
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Murinae; Mus
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FEATURES

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Collection (MGC)

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US-10-627-571-2 (1-188) x BI688217 (1-908)
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                                                                                                                                                                                                           LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
                                                                                                                                                                                                                                                                             MetThrValValSerPheHisGlnValAspTyrThrPheAspArgAsnValLeuSerArg
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     LysMetLeuAspGluGluAsnIle
                                                                                                                                              SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla 160
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                                           TTGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGGCCTCAAC
                                                                  LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn
                                                                                                                 TCTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGATTGTGATTCTTTGGCTGCC
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
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/mol_type="mRNA"
/strain="FVB/N"
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/tissue_type="infiltrating
/dev_stage="5 months"
/lab_host="DH10B"
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/clone="IMAGE:5354452"
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61 LysIleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGln
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Tissue Procurement: Jeffrey Green M.D.
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National Institutes of Health, Mammalian
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1 (bases 1 to 766)
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/tissue_type="infiltrating
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/strain="FVB/N"
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BI103517
BI103517.1 GI:14554410
EST.
Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                      late: LLAM11121 row: c column: igh quality sequence stop: 751.
Location/Qualifiers
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                                                                                                                           /db_xref="taxon:10090"
/clone="IMAGE:5044167"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                 strain="FVB/N"
 3.52e-99
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                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) wit.
and advice from Piero Carninol (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAM363 row: 1 column: 23
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CB991862.1
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 785)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
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AGENCOURT 13618130 NIH MGC 148 Homo
IMAGE:30337918 5', mRNA sequence.
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                                                         nLysMetLeu-AspGluGlu 186
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                                           CAAAATGTTGGGATGAAGAG
                                                                                                  TTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGGTGATGGTATCAA
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/clone lib="NIH MGC_148"
/clone lib="NIH MGC_148"
/note="Organ: placent; Vector: pBluescriptR; Site all-KhoI; Site 2: BamH; Library is oligo-dT primed directionally Cloned using primer
5'-TTTTTTTTTTTTTTTTTVN-3', size-selected for average
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30337918"
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Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Instituphysical and Chemical Research (RIKEN), Laboratory for Genexploration Research Group, RIKEN Genomic Sciences Center RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Haradda, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Gro
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High-efficiency full-length cDNA cloning
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Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/.
URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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CTTGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGGCATCAA
               aLeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAs
                                                                                        GCTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAA
                                                                                                    gLeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLy
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/clone_lib="RIKEN full-length
/dev_stage="0 day neonate"
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/mol_type="mRNA"
/strain="C57BL/6J"
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Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
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/mol_type="mRNA"
/mol_type="mRNA"
/db_xref=""exaxon:9606"
/tissue_type="normal nasopharynx"
/clone_Tib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx
library from southern Chinese"
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sapiens cDNA, mRNA sequence
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Homo.
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1 (bases 1 to 656)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://image.llnl.gov
Plate: LLAM11900 row
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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BI687787
BI687787.1 GI:15650415
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603314107F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354281 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tissue Procurement: Jeffrey Green M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                          MetAlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeu
 GGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCGAGGTG
                       GlyLysMetValSerLysSerIleAlaThrThrLeuIleAspAspThrSerSerGluVal
                                                                       GTGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCACATGGACGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCC 564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence stop: 632.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             /clone_lib="NCI_CGAP_Mam6"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                               dev_stage="5 months"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="IMAGE:5354281"
sex="female, virgin"
tissue_type="infiltrating ductal carcinoma"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus")
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98.92%
93.51%
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                                                                                                                                                                                            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469E2119
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                    Pongo pygmaeus mRNA
Unpublished (2004)
Contact: MIPS
                                                                                                                                                                                                                                                                                       Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wie Molecular Genome Analysis, German Cancer Research Center (DKF Email, s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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DKFZp469E2119_5', mRNA sequence.
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Mewes, H.W., Weil, B., A
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Pongo pygmaeus
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/mol type="mRNA"
/db_xref="taxon:9600"
/clone="DKFZp469E2119"
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/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Si
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EST 13-JUL-2004 s cDNA clone

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Wellenreuther,R., G., Han,M. and

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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, I
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                     Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clinglingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.B., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                   CV023086 The mrnA linear EST 20-AUG-2004 S463 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC007014, mrnA sequence.
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 566)
                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens cDNA
CV023086
                                                                                                          Contact: Vidal M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each clresults from a PCR reaction using an MGC full-length cDNA template DNA and ORF specific primers
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 566 Std Error: 21.00
Plate: 11075 row: 05 column: F
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
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BACKWARD: CATATGTTCTCTTCATCCAACATTT
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                                                             SerHisGlyArgValAsnAsnValPheAspHisPheSerAspCysGluPheLeuAlaAla
                                                                                                                                              LeuLeuAsnGluCysArgGluMetLeuHisGlnIleIleGlnArgHisLeuThrAlaLys
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                                                                                                                         CTGTTANATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
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                                      TCACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib='Collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol type="mrNa"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_lib="Full Length cDNA from the Mammalian
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TITLE
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183
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODE013CE09QP1&c=3485.f.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EV
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Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30548565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates;
1 (bases 1 to 779)
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                                                                                                                                                                                                                                                     AlaThrAspValPheAsnSerLysAsnLeuAlaValGlnAlaGlnLysLysIleLeuGly
                                                                                                 AspGluLeuTyrArgValThrArgGluTyrThrGlnAsnLysLysGluAlaGluLysLys 61
                                                                                                                                                    AAAAWGGTGTCCAAATCCATCGCCACCACCTTAAWARAMGACACAAGTAGTGAGGTGCTG
                                                                                                                                                                                                                               ATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAAWCAGTTT
                      IleLysAsnLeuIleLysThrValIleLysLeuAlaIleLeuTyrArgAsnAsnGlnPhe 81
                                                                         GATGAGCTCTACARAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="CS0DE013YJ17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Homo sapiens"
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898.00
95.19%
95.19%
93.35%
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Matches:
Conservative:
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Indels:
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cDNA clone CS0DE013YJ17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 747)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CD520304 747 bp n
AGENCOURT 14360208 NIH MGC 191 Homo
IMAGE:30410510 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: CLONTECH Laboratories, IncDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution informat:
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                                                                                                                                                                                                                                                                                                                                                                                    e: NDCM200 row: m column: 15 quality sequence stop: 499. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens (human)
/clone="IMAGE:30410510"
/tlissue_type="pooled"
/lab host="DH10B (TI phage-resistant)"
/lab host="DH10B (TI phage-resistant)"
/clone lib="NIH MGC 191"
/clone lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);
/ite 2: SfiI (ggccgctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/shour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69
kb (range 0.70-5.0.kb). 15/15 colonies contained inserts
                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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VERSION
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                  RESULT 43
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                                                                                                                                                                                                                                                                        BY743355
BY743355
                                                                                        Mus musculus (house mouse)
Mus musculus
Mus musculus
Eukazyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukazyota, Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                            musculus cDNA clone I83
BY743355
BY743355.1 GI:27169364
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                            LysMetLeu 183
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                                                                                                                                                                                                                                                671 bp mRNA linear
RIKEN full-length enriched, bone marrow
cDNA clone I830007M06 5', mRNA sequence.
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893.00
97.27%
96.17%
92.83%
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Matches:
Conservative:
Schriml, L.M., Kanapin, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                          linear
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                    Bult, C.
                                                                            Kondo, S.,
                                                                                                                  Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                   prepare mouse tissues.

Tissues were provided by David A. Hume ( Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Tel: 81-45-503-9222
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Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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                                               /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                         organism="Mus"
                                                                                                                                                                                                                                                                         Location/Qualifiers
db_xref="taxon:10090"
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          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (Dases 1 to 739)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                    Mus
                                                                                                          mRNA sequence. — — BF140519 BF140519.1 GI:10979546 EST.
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601787536F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015160 5',
Email: cgapbs-r@mail.nih.gov
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/clone_lib="RIKEN full-length
macrophage"
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by:Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM9260 row: h column: 09
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LysMetLeuAspGluGluAsnIle 188
                                  LeuTyrAsnProPheGlyAsnPheLysProHisLeuGlnLysLeuCysAspGlyIleAsn 180
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Location/Qualifiers
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/lab_host="PH108"
/clone_lib="NCI_CGAP_Lu30"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; transgenic model wNT-1, expression dr.
MMTV-LTR enhancer; Cloned unidirectionally. Primer dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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/strain="CZECH II"
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Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

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AX097884 Homo sapi
AC093257 Rattus muscu
BC009090 Mus muscu
AC120859 Mus muscu
AC120859 Mus muscu
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AC160859 Sequence
CR760636 Kenopus I
BC072904 Kenopus I
BC072965 Sequence
CR8446252 Sebrafish
AC012678 Homo sapi
AC012678 Homo sapi
AC012678 Homo sapi
AC013505 Rattus no
BC0127940 Rattus no
BC0127940 Rattus no
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CR407586 Danio rer
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BC052338 Danio rer
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AC073688 Mus muscu
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AC073689 Mus muscu
AC073690 Rattus no
BC017712 Homo sapi
BC017712 Homo sapi
BC017712 Homo sapi
AX078255 Sequence
AX182911 Homo sapi
AX078256 Papio anu
AC111709 Rattus no
BC0171109 Rattus no
BC0171109 Rattus no
BC0171109 Rattus no
BC079119 Mus muscu
AC111709 Rattus no
BC079119 Aus muscu
AC111709 Rattus no
BC079119 Aus muscu
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AC111709 Rattus no
BC079119 Fapio anu
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BC07917174 Homo sapi
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Direct Submission
Submitted (05-JUN-1998) Biochemistry, Ac
Meibergdreef 15, Amsterdam 1105 AZ, The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1892)

Horrevoets,A.J., Fontijn,R.D., van Zonneveld,A.J., de Vries,C.J., ten Cate,J.W. and Pannekoek,H.

Vascular endothelial genes that are responsive to tumor necrosis factor-alpha in vitro are expressed in atherosclerotic lesions, including inhibitor of apoptosis protein-1, stannin, and two nove
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                                    CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                          AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                           AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                                                                    CTTCAGCGTCCCCGGCCCCCCCCCCCCACAGATGTCTTTAATTCCA
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/kvtreytqnkkeaeklikuliktviklailyrnnqfnqdelalmekfkkkvhqlamt
VvsehqvDytpedrnvlastllaecremliqiiqRhltakshgrvnnvfdhfsdceflaa
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/protein_id="AAC83229.1"
/db_xref="GI:3978238"
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                                                                                                                                                                                                                                                                                                                                                                                                               cell_type="endothelial"/tissue_type="umbilical
                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
mol_type="mRNA"
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                                                                                                   and Ni,J.

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110 human secretory proteins Patent: UP 2002508167-A 107 19 HUMAN GENOME SCIENCES INC OS Homo sapiens (human) PN JP 2002508167-A/107 PD 19-MAR-2002 G0/070 9 18-DEC-1997 US 60/068 057,18 18-DEC-1997 US 60/068 008,18 18-DEC-1997 US 60/068 008,18 18-DEC-1997 US 60/068 169,19 19-DEC-1997 US 60/068 367,19 19-DEC-1997 US 60/068 365 PI DAUL A MOORE, STEVEN M RUB-PI A ROSEN,
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PI FORD J
PC C12N15
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                                                       PI DANIEL R SOPPET, HARA ROSANNE D DUAN,
PI CHARLES FLORENCE, JOHN
LIANG YU,
                                                                                                                                                                                                                                                                                                                                                                            Moore, P.A., Ruben, S.M., Carter, K.C., Shi, Y., Roy Soppet, D.R., Caou, H., Wei, Y.F., Florence, K., Duz Florence, C., Greene, J.M., Feng, P., Perrie, A.M.,
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110 human secretory proteins.
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                            C12N15/09, A61K38/00, A61K48/00, A61P9/00, A61P9/10, A61P15/00,
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FORD JANAT, JIAN
                                                                                                     R SOPPET, HARA CAOU, YING
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G0/070 923,18-DEC-1997 US 6

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Duan, R.D.,
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A61P29/00,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/
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                                                                                                              TTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA
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Location/Qualifiers
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/mol_type="genomic DNA"
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Pred. No. 2.4e-136;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1921)
Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J.
Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T.
Primer for synthesizing full-length cDNA and use thereof
Patent: JP 2002191363-A 11723 09-JUL-2002;
HELIX RESEARCH INSTITUTE
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Primer for
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                                                                                            TTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTA
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JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU
KEIICHI NAGAI,TETSUJI OTSUKI
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28-JUL-2000 JF 2000280990
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU
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JP 2002191363-A/11723
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                               Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuk. Nishikawa,T., Nagqi,K., Sugano,S., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Sasaki NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                          Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S. Complete sequencing and characterization of 21,243 full-length
3 (bases 1 to 1921)
Isogai,T. and Otsuki,T.
Direct Submission
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BD156785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  etc.) and Department of Virology, Institute of Medical Science, University of Tokyo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                 601
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/tissue_type="placenta"
/clone_lib="pLACE1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="cloning vector: pME18SFL3"
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99.5%;
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Pred. No. 5.3e-136;
0; Mismatches 2;
 1729
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                                                                                                                                   396 TGTTAAATGAATGCAGAGAGAGTGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                                                                                      336 TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGC
                                                                                                                                                                                                                                                                                               276
516 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA 575
                                                                                                              462
                                                                                                                                                                                   402
                                                                                                                                                                                                                                                          342 TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
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                                                                                                                                                                                                                                                                                                                                                                      216
                                                                                                                                                                                                                                                                                                                                                                                                           222 TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 GTANAATGGTGTCCANATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1729)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 11628 09-JUL-2002; HELIX RESEARCH INSTITUTE

OS Homo sapiens (human)
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Primer for_
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BD156785
BD156785.1 GI:27862543
JP 2002191363-A/11628.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity 99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10,
                                                                                                                                                                                                                                                                                                                                  TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                       CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                                                   TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                                                                                                                                                TTAATCAAGATGAGCTAGCATTGATGGAGAAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-2002
28-JUL-2000 JP 2000280990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JP 2002191363-A/11628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 564.4;
Pred. No. 2.2e
0; Mismatches
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581 515 521 455 461 401 335 341 275

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Key ဥ

94 GTAAAATGGTGTCCAAATCCATCGCCACCACCATAATAGACACACAAGTAGTAGTGAGGTGC 155	/not /coc /coc /coc /coc /prc /prc /db /cra /cra DTSS KKKW HFSE Conserva s 565; Conserva 36 TGGCCACAGAT	O Z	Db 582 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGTAATCAACA 641 Qy 576 AAATGTTGGATGAAGAGAACATATGA 601 Db 642 AAATGTTGGATGAAGAGAACATATGA 667 RESULT 7 AX877673 LOCUS AX877673 DEFINITION Sequence 12578 from Patent EP1074617. ACCESSION AX877673 ACCESSION AX877673
Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S. Complete sequencing and characterization of 21,243 full-length human cDNAs JOURNAL Nat. Genet. 36 (1), 40-45 (2004) PUBMED 14702039 REFERENCE 2 AUTHORS Isogai,T., Ota,T., Hayashi,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nagai,K., Sugano,S., Takahashi-Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamanoto,J., Wakamatsu,A., Nabemura,Y., Nagahari,K., Masuho,Y. and Oshima,A. NIPHORS Isogai,T. and Otsuki,T. AUTHORS Isogai,T. and Otsuki,T. Suguno,S., Takanashi-Fujii,A., Hara,H., Tanase,T., Nabehura,T., Ishii,S., Kawai,Y., Saito,K., Yamanoto,J., Wakamatsu,A., Nabehura,T., Nagahari,K., Masuho,Y. and Oshima,A. DOURNAL Unpublished 3 (bases 1 to 1729) Isogai,T. and Otsuki,T. Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	Shiratori, A., Sudo, H., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Kanda, K., Yokoi, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamihara, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, M., Yamazaki, M., Ninomiya, K., Ishibashi, T., Yamashita, H., Murakawa, K., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, S., Yosida, M., Hocuta, T., Kusano, J., Kanehori, K., Takahashi-Fujii, A., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuuki, H., Oshima, A., Sasaki, N., Aotsuka, S., Yoshikawa, Y., Matsunawa, H., Ichihara, T., Shiohata, N., Sano, S., Moriya, S., Momiyama, H., Satoh, N., Takami, S., Terashima, Y., Suzuki, O., Nakagawa, S., Senoh, A., Mizoguchi, H., Goto, Y., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, K., Kumagai, A., Tlakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Tashiro, H., Tanigami, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T., Okamoto, S., Okitani, R., Kawakami, T., Kobatake, N., Inagaki, H., Ikema, Y., Okamoto, S., Okitani, R., Kawakami, T.,	RESULT 8 AKO01850 AKO01850 AKO01850 AKO01850 AKO01850 DEFINITION Homo sapiens cDNA FLJ10988 fis, clone PLACE1001920, highly similar to Homo sapiens MDC-3.13 isoform 2 mRNA. ACCESSION ACC	QY 456 CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTTTTGGCTGCCT 515

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J.K., Katsuta, N., Sato, K.,
Ishibashi, T., Yamashita, H.,
Imata, M., Watanabe, M.,
Y., Takiguchi, S., Watanabe, S.,
hori, K., Takahashi-Fujii, A.,
S., Komai, F., Hara, R.,
S., Komai, F., Hara, R.,
Shino, K., Yuuki, H., Oshima, A.,
Matsunawa, H., Ichihara, T.,
yama, H., Satoh, N., Takami, S.,
Senoh, A., Mizoguchi, H.,
gaki, H., Watanabe, T.,
yaki, H., Watanabe, T.,
yaki, H., Watanabe, T.,
yaki, H., Watanabe, T.,
yaki, H., Watanabe, T.,
na,T., Otsuki,T., Suzuki,Y.,
cahashi-Fujii,A., Hara,H.,
.F., Hara,R., Takeuchi,K.,
.Y., Saito,K., Yamamoto,J.,
, Masuho,Y. and Oshima,A.
                                                                                                                                                                                                                             .T., Matsumura,K.,
asaki,M., Togashi,T.,
u,T., Mizushima-Sugano,J.,
agawa,K., Okumura,K.,
ho,Y., Yamashita,R.,
O., Isogai,T. and Sugano,S.
on of 21,243 full-length
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Ujimori,Y., Komiyama,M.,
Ono,T., Yamada,K., Fujii,Y.,
a,A., Hikiji,T., Kobatake,N.,
ani,R., Kawakami,T.,
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,Y., Isono,Y., Nakamura,Y.,
wayanagi,T., Wagatsuma,M.,
u,Y., Kodaira,H., Kondo,H.,
okoi,T., Furuya,T.,
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ACE1001920, highly similar
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.; Hominidae; Homo.
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Homo.

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KEYWORDS
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                                                                                                                     5352 1814 bp mRJ sapiens tumor necrosis factor, a. A. clone MGC:12451 IMAGE:3997650),
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="cloning vector: pME18SFL3"
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clone_lib="PLACE1"
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Stheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: b Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.(B.E. Consortium (LLLL) DNA Sequencing System Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC Project URL: http://r
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dickson, M., Schmutz, J., Grimwood, J., Rodriquez,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                            /gene="TNFAID8"
/note="synonyms: GG2-1, l
/db_xref="LocusID:25816"
144. .740
                                                                                                                                                                                                                                                                                                                                                    /clone="MGC:12451 IMAGE:3997650"
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                                                                                                                                                                                                                                                                                                          'note="Vector:
                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www-shgc.stanford.edu (Dickson, Mark) mcd@paxil.stanford.edu
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Homo sapiens l
AF099935
AF099935.1 G
    2 (bases 1 to 1915)
Nietfeld, W. and Meye
                                             Nietfeld, W. and Meyerhans, A.F. Identification of cellular factors of dendritic cells
                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 1915)
                                                                                                                                             Homo
                              Unpublished
                                                                                                                                Homo sapiens
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                                                                                                                                             sapiens (human)
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/note="DUF758, Region: Domain of unknown function
(DUF758). Family of eukaryotic proteins with unknown
function, which are induced by tumour necrosis factor"
/db_xref="CDD:pfam05527"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKKVHQLAMTVVSFHQVDYTFDRNVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFD
HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
180. .737
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Catarrhini; Hominidae;
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Submitted (13-OCT-1998) Max Planck Institute for Submitted (13-OCT-1998) Max Planck Institute for Genetics, Thesstrasse 73, Berlin 14195, Germany Location/Qualifiers
1. .1915
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nilarity 99.8%;
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DTSSEYLDELYRVTREYTQNKEAEKIIKNLKTVIKLAILYRNNQFNQDELALMEKF
KKKYHQLAMTVVSFHQNDYFEDRNVLSRLLABECREMLHQIIQRHLTAKSHGRVNNVFD
HFSDCEFLAALYNPFGNFKPHLQKLCDGINKMLDEENI"
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/protein_id="AAC72975.1"
/db_xref="GI:3860093"
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IL-4"
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/db_xref="taxon:9606"
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/codon_start=1
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   Homo
                                   Homo sapiens MDC-3.13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent: WO 02068579-A 12009 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majo humanexons or transcripts, for detecting expression
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Homo sapiens
Eukaryota; Metazoa;
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sapiens
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/mol_type="unassigned DNI
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Best Local Similarity
Matches 565; Conserv
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336 TGACCGTGGTCAGTTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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1 (bases 1 to 2003)
Nietfeld, W. and Meyerhans, A.F.
Identification of cellular factors involved in the differentiation of dendritic cells
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Nietfeld, W. and Meyerhans, A.F.
Direct Submission
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                                                              TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
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/codon_start=1
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ELYRVTREYTQNKKEREKIIKNLIKTVIKLAILYRNNQFNQDELALMEKFKKKVHQLA
MTVVSFHQVDYTFDRAVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFDHFSDCEFL
AALYNPFGNFKPHLQKLCDGINKMLDEENI"
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/db xref="taxon:9606"
/cell_type="adherent "
IL-4"
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Klausner, R.D., Collins, F.S., Wagmer, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Bouffard, G.G., Blakesley, R. W., Touchman, J.W., Green, E.D.,
Dickeon, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Dickeon, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 16 Row: b COlumn: 7
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657123.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: CLOMTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (30-APR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZUBL DD MRNA linear PRI 24-FEB-20.
Homo sapiens tumor necrosis factor, alpha-induced protein 8, mRNA (cDNA clone MGC:12346 IMAGE:3930240), complete cds.
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R. M.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                    /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                               /tissue_type="Brain, primitive
/clone_lib="NIH_MGC_56"
note="Vector: pDNR-LIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
4., Schmutz, J., Grimwood, J., Rodrique
                           lab_host="DH10B"
                                                                                                                         clone="MGC:12346 IMAGE:3930240"
                                                                                           neuroectodermal"
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                                                                                         TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                                                           CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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                                                                    TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                         CACATGGACGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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/note="synonyms: GG2-1, MDC-3.13, SCC-S2"
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237. .833
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KKKVHQLAMTVVSFHQVDYTFDRNYLSRLLAMECREMLHQIIQRHLTAKSHGRVNNVFD
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KKKVHQLAMTVVSFHQVDYTFDRNYLSRLLAMECREMLHQIIQRHLTAKSHGRVNNVFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TNFAIP8"
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AK097284 2502 bp mRNA linear Homo sapiens cDNA FLJ39965 fis, clone SPLEN2027157, to Homo sapiens MDC-3.13 isoform 2 mRNA.

PRI 30-JAN-2004 highly similar

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TITLE
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AUTHORS
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                                                                                                                                                                                                                            Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB.
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Isogai,T. and Yamamoto,J.
Direct Submission
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/db_xref="taxon:9606"
/clone="SPLEN2027157"
                                                                          organism="Homo sapiens"
|mol_type="mRNA"
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                            Submitted (06-APR-2000) Production Sequencing Facility, Genome Institute, 2000 Mitchell Drive, Walnut Creek, CA (Dases 1 to 112626)

DOE Joint Genome Institute and Stanford Human Genome Ce
                                                                                            2 (bases 1 to 112626)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 112626)

DOE Joint Genome Institute and Stanford Human Genome Center.
Submitted (27-APR-2001) DOE Joint Genome Institute,
                  Direct Submission
                                                                                                                                                            Direct Submission
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                                                                                                                                           Unpublished
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/note="cloning vector: pME18SFL3"
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On Apr 27, 2001 this sequence version replaced gi:7712094.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Pinishing Completed at Stanford Human Genome Center
www-shgc.stanford.edu
Ouality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
     Homo
                                 Homo sapiens chromosome
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AC026795.6 GI:15718543
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/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2220M12"
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Submitted (31-AUG-2001) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA 4 (bases 1 to 156277)
DOE Joint Genome Institute and Stanford Human Genome Direct Submission
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DOE Joint Genome Institute and Stanford Human Genome Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (21-SEP-2001) DOE Joint Genome Institute, 2800 Mi
Drive, Walnut Creek, CA 94598, USA
On Sep 21, 2001 this sequence version replaced gi:15383783
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
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Submitted (24-MAR-2000) Production Sequencing Facility, DOE Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 9459
3 (bases 1 to 156277)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                              Finishing Completed at Stanford Human Genome C
www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.4.
STS Content:
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DOE Joint Genome Insti
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/mol_type="genomic DNA"
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                     clone="CTD-2287L22"
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Score 564.4; DB 9;
Pred. No. 2.4e-130;
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Research Shizuya et Kim et al.,

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                                                                                                                                                                                           all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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                                                         MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-JAN-2003) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 158057)
Tomlinson, C. and Bielicki, L.
The sequence of Homo sapiens
Cupublished (2001)
    SOURCE INFORMATION:
Clone CTD-2293E22 i
                                                                                                                                                                                                                                                                                            This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (30-MAY-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                   restriction
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) 99063792
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Sulston, J.E. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 158057)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: H_MS2293E22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Sequencing Center Center code: WUGSC
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This sequence is the entire insert of
Location/Qualifiers
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7920. .8106
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2532. .257s
/rpt_family="polypurine"
20419. .20468
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4351. 4541
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6329. .7499
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1964. .1996
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19548. .19664
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2859. .2886
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L8238 . 18436
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L5534. .17744
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[225]. .12442
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7503. .7872
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1518. .1547
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|321. .1459
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37311. .37413
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35523. .35598
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33458. .33570
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29871. .30008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            573 bp mRNA linear PRI 03-JUN-200 Homo sapiens full open reading frame cDNA clone RZPDo834H127D for gene TNFAIP8, tumor necrosis factor, alpha-induced protein 8; complete cds, incl. stopcodon. CR457137
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 573)

Ebert, L., Schick, M., Neubert, P., Schatten, R., Henze, S. and Korn, B. Cloning of human full open reading frames in Gateway (TM) system
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
                                                                                                                  RZPD; RZPDo834H127D, ORFNo 1910
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPDo834H127D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No
                                                                                                                                                                                                                                                                                     entry vector (pDONR201)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR457137.1 GI:48146390 Full ORF shuttle clone, Gateway(TM), complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA 134928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contact RZPD (customer.service@rzpd.de) for further information. This CDS clone is a part of a collection of human full length expression clones generated by RZPD.

This CDS has been cloned incl. stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase (TM)

Teaction. Additional sequence has been added in front of the start codon: att. AAAAAA GCA (GGC (ATG).

The last base of the last coding triplett has been changed to T, which might lead to an amino acid change at the C terminus of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAACCCAGCTTTCTT. .att. Compared to the reference sequence NM_014350 we did not find any amino acid exchanges.

Clone distribution: http://www.rzpd.de/products/orfclones/.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The stop codon has been set to TAA followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAAAATGGTGTCCAAATCCATCGCCACCCTTAATAGACGACACAAGTAGTGGGGTGC
CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
                                                                                                                                                                    TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                                                                                                       TTÄATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTA
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                                          TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                            TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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/db xref="GI:48146391"
/db xref="GI:48146391"
/trānslation="MANATDVFNSKNLAVQAQKKILGKMVSKSIATTLIDDTSSEVLD
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MTVVSFHQVDYTFDRNVLSRLLNECREMLHQIIQRHLTAKSHGRVNNVFDHFSDCEFL
AALYNPFGNFKPHLQKLCDGINKMLDEENI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/clone="kzPp0834H127D"
/clone_lib="Human Full ORF Clones Gateway(TM) -
/lab_host="DH10B"
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Pred. No. 1.3e-129;
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                                                                                                                                          156 TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCCAAAACAAGAAGGAGGAGAGAAGA
276 TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA 335
                                                                                                                                                                                            162 GTAAAATGGTGCCAAATCCATCGCCACCCTTAATAGACGACACAAGTAGTGAGGTGC
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                                                                                                                                                                                                                                                                                                                                                     562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 816)

Ota, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J. Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002191363-A 4238 09-JUL-2002;

HELIX RESEARCH INSTITUTE
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                                                                             TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                   TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA
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JUNICHI YAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU,
KEIICHI NAGAI, TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C12P21/02, C12Q1/68//C12P21/08, G06F17/30, C12N15/00, C12N5/00
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28-JUL-2000 JP 2000280990
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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36 TGGCCACAGATGTCTTTAATTCCAAAAACCTTGGCCGTTCAGGCACAAAAGAAAG	AX869333 Sequence 4238 from Patent EP107 AX869333 AX869333.1 GI:40024196 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; C Mammalia; Eutheria; Primates; C 1 Ota,T., Isogai,T., Nishikawa,T. Ishii,S., Sugiyama,T., Wakamate primers for synthesising full.l Patent: Ep 1074617-A 4238 07-FE Research Association for Biotec Location/Qualifiers e /organism="Homo sapier /mol_type="unassigned /db_xref="taxon:9606" tch l Similarity 98.9%; pred. No. 562; Conservative 0; Mismat	516 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAACTATGTGATGGTATCCAACA 575	ν σ	TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT	
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Best Local Similarity 93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Isogai, T.
NEDO human cDNA sequencing project
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and Isogai,T.
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Isogai, T. and Yamamo
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                   AACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATAT
                                                                                                            TTGATCATTTTTCAGATTGTGAATTTTTTGGCCTGCCTTGTATAATCCTTTTTGGGAAATTTTA
                                                                                                                                                                 TGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGT
                                                                                                                                                                                                                                                                                  TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
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AACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATAT
                                                                                                                                                                                                TGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCT
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYMU2004688"
/tissue type="thymus"
/clone_lib="THYMU2"
/note="cloning vector: pME18SFL3"
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                                  Worley, K.C.
Direct Submission
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Rattus norvegicus
Submitted (16-SEP-2001) Human Genome Sequencing Center, Department
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html

* NOTE: This is a 'working draft' sequence. It currently

* consists of I contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 237561: contig of 237561 bp in length.

1 cocation/Qualifiers
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Baylor Plaza,
3 (bases 1 tc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baylor Pla
On Nov 9,
The sequen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular and Human Genetics, Bay
ylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lor Plaza, Houston, TX 77030,
(bases 1 to 237561)
t Genome Sequencing Consortium.
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vlor Plaza, Houston, TX 77030,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GDPL

Center clone name: CH230-10A12

Center clone name: CH230-10A12

Center clone name: CH230-10A12

Center clone name: CH230-10A12

Resembly program: Phrap; version 0.990329

Consensus quality: 229749 bases at least Q40

Consensus quality: 231209 bases at least Q30

Consensus quality: 231209 bases at least Q20

Estimated insert size: 232575; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence in this assembly is a combination of BAC based
                                                                                                                                             /note="wgs contig"
complement(232422...2
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_end_extension clone_end:Sp6"
                                                                                                                                                                                                                                                             end_sequence:BH303075"
76320. .79576
clone
                                                      end_sequence:BH303071"
234103. .235440
                                                                                                                  site:EcoR
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                                                                                                                                                                                                                                                                                                                                           6006. ...6586
/note="clone_boundary
clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- Genome Center
'note="wgs_end_extension
:lone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="CH230-10A12"
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Best Local
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                     Strausberg, R. I., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausmer, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.I. Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K. Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Millahy, S.J., Bosak, S.A., 
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 1728)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC009090 1728 bp mRNA linear ROD 30-JUN-2004 Mus musculus tumor necrosis factor, alpha-induced protein 8, mRNA (CDNA clone MGC:11714 IMAGE:3965693), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
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McKernan, K.J., Malek, J.A., Gunaratne, P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC009090.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAGGTGCACCAGCTGGCCATGACGGTGGTGAGCTTTCACCAGGTAGAGTACACCTTTG
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/note="wgs_end_extension
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85.9%;
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Pred. No. 9.4e-103;
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Best Local Similarity
Matches 490; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 17 Row: n Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 195273.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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73.9%; ilarity 86.6%; Conservative
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                                                                                                                                        /db_xref="locusID:106869"
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/db_xref="MGI:2147191"
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/db_xref="MGI:2147191"
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model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI_CGAP_Mam1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="Tnfaip8"
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/clone="MGC:11714 IMAGE:3965693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="FVB/N"
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   <u>,,</u>
Score 444.4; DB 10;
Pred. No. 2.3e-100;
0; Mismatches 76;
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Indels
                                                   Length 1728;
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REFERENCE
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cock, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., God, S., Goyette, M., Graham, L., Grand-Pierre, N., Ginde, S., God, S., Goyette, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (Dases 1 to 184327)
Birren,B., Nusbaum,C. and Lander,E.
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AC120859
                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE AUTHORS
MCCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oilver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Venkataraman, V.S., Viel, R., Direct Submission Submitted (05-AUG-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 5, 2004 this sequence version replaced gi:49035085. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zomber, A. and Zody, M. Direct Submission Submitted (22-UN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 184327) Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., Fitzderald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagos, B., Hall, J., Horton, L., Hulme, W., Illey, I., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabithews, C., MacGonald, P. C., Marcon, J., Manning, J., Mastthews, C., MacGonald, P., Major, J., Manning, J., Markethews, C., MacGonald,	Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M. Direct Submission AL Distance Street, Cambridge, MA 02141, USA Submitted (13-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA Ghases 1 to 184327) Sirren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N., Anderson,M., Anderson,S., Arachchi,H.M., Barna,M., Bastien,V., Bizren,B., Nusbaum,C., Lander,E., Cooke,P., Corum,B., Bloom,T., Bouslavky,I., Boukhgalter,B., Camarata,J., Chang,J., Chapel,Y., Collymore,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S., Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B., Liu,G., Liu,X., Lui,A., Mabbitt,R., Maclean,C., Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M., Meldrin,J., Meneus,L., Mihova,T., Mlenca,V.,
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Submitted (20-MAY-2004) Caldwell R.B., GSF
Submitted (20-MAY-2004) Caldwell R.B., GSF
Institut fuer Molekulare Strahlenbiologie,
1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezzubov,Y., Zaim,J., Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter,M., Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M. Full-length cDNAs from bursal lymphocytes to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus
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ORF1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2009)
Caldwell,R.B.
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                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function analysis
                         AGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATC
                                                                     TTTTAGATGAGCTCTACAGAGTGACGAAGGAATACACGCAAAACAAAAAAGAAGCAGAGA
                                                                                                    TGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGA
                                                                                                                                       TTGGGAAAATGGTATCCAAGTCAATAGCAACTACTTTGATAGATGATACCAGCAGTGATG
                                                                                                                                                                  TGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGG
                                                                                                                                                                                                           CAATGGCCACGGATGTCTTCAATTCAAAAAAGCTTGGCCATTCAGGCCCAGAAGAAGATCC
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="matdvfnskslaiqaqkkiigkmvsksiattliddtssdvldel
yrvtkeytqnkkbabkiiknlikivlklailyrnnqfnqdeialmekfkkkvhqlakt
vvsfhqvdytfdrnflskllndcrellhqiiqrhltakshgrvnnvfdhfsdceflaa
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189. .755
                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="RCJMB04_29h8"
                                                                                                                                                                                                                                                                                                                                                                                                       LYNPFGPYKLHLOKLCDGVNRMLDEGNI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (codon start=1)
(product="hypothetical protein"
(protein id="CAG32565.1"
(db_xref="GI:53136472"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphocyte"
/tissue_type="bursa"
/clone_lib="riken1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Gallus gallus"
|mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                locus_tag="RCJMB04_29h8"
note="ORF1"
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Pred. No. 2.1e-91
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    Forschungszentrum,
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426
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PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers FT source 1.587 FEATURES Location/Qualifiers 1.587 FEATURES Location/Qualifiers Source /organism="Homo sapiens (human)' /organism="Homo sapiens" /organism="Homo sapiens (human)' FEATURES FT Location/Qualifiers /organism="Homo sapiens (human)' /organism="Homo sapiens" /organism="Homo sapiens" /organism="Homo sapiens (human)' /organism="Homo sapiens (human)' /organism="Homo sapiens (human)' /organism='Homo sapiens (human)' /organism="Homo sapiens (human)' /organism='Homo sapiens (human)' /organ	SOURCE Homo sapiens (human) ORGANISM Homo sapiens (human) ORGANISM Homo sapiens (Exercise Primates) Extracycta; Metazoa; Chordata; Craniata; Vertebrata; Exteleostomi; REFERENCE 1 (bases 1 to 587) AUTHORS Cta, T., Isogai, T., Nishikawa, T., Hayashi, K., Saito, K., Yamamoto, J., Ishii, S., Sugiyama, T., Wakamatsu, A., Nagai, K. and Otsuki, T. Primer for synthesizing full-tength cDNA and use thereof Patent: JP 2002191363-A 4476 09-JUL-2002; HELIX RESEARCH INSTITUTE OS Homo sapiens (human) PN JP 2002191363-A/4476 PD 09-JUL-2002 PF 28-JUL-2002 PF 28-JUL-2002 PF 28-JUL-2003 JP 2000280990 PI TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, KOJI HAYASHI, KAORU PI SAITO, PAMAMOTO, SHIZUKO ISHII, TOMOYASU SUGIYAMA, AI WAKAMATSU, PI KEIICHI NAGAI, TETSUJI OTSUKI CLANIS/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC	CY 5/3 ACAAAATGTTGAAGAGAACATAT 599 CY 5/3 ACAAAATGTTGAAGAGAACATAT 599 Db 727 ACAGAATGCTAGATGAAGAGGGAACATAT 753 RESULT 26 BD149633 LOCUS BD149633 LOCUS BD149633 DEFINITION Primer for synthesizing full-length cDNA linear PAT 17-JAN-2003 DEFINITION BD149633 VERSION BD149633 VERSION BD149633 GI:27855391 KEYWORDS JP 2002191363-A/4476.	453 AGTCACATGGACGGGTTAATAATGTCTT	Qy 273 AGTTTAATCAAGATGAGCTAGCATTGATGAGAAAATTTAAGAAGAAAGTTCATCAGCTTG 332
Query Match 65.7%; Score 394.6; DB 6; Length 587; Best Local Similarity 96.6%; Pred. No. 6.5e-88; Matches 422; Conservative 0; Mismatches 13; Indels 2; Gaps 2; Qy 1 CTTCAGCGTCCCGGGGGCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTAATTCCA 59	EP1074617 ta; Crani es; Catar wa,T., Ha all-lengt 07-FEB-20 10teChnol rs gned DNA" 606"	Oy 36 TGANTATACCTTTGACCGAATGTGTTAAATGAATGCAG-AGAATG 418 6	TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA	OY 1

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                                                                                                                                                                                                                                                                                                                                                          452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (15-SEP-2004) Sanger Institute, Hinxton, Cambridgeshi CB10 1SA, UK. E-mail enquiries: trop@sanger.ac.uk Sanger Xenopus tropicalis EST/CBNA project.

This sequence is from a Xenopus Gene Collection (XGC) library, a library constructed by Aaron M. Zorn. cDNA was prepared from extracted from eggs. EcoRI-NotI cDNA was then ligated into pCS107 with EcoRI at the 5' end and NotI at the 3' end.

Vector: pCS107; Site 1: EcoRI; Site 2: NotI Host: Escherichia coli XII-blue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                     GTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG---TGTCCAAAATCCATCGCCACCACC 127
                                                                                                                  TTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTAC
                                                                                                                                                                              GTACAAGCCCAAAAGAAGATTCTTGGCAAGATGGCCTCATCAAAGTACATAGCAACATCC
                                                                                                                                                                                                                                                                 CCCGCTCCGAGCGCCACTGAGCCAATGGCAACAGATGTCTTCAGTTCCAAAAAATCTGGCT 190
                                                                                                                                                                                                                                                                                                        CCGGCGCCGTCGCCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCC 70
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                                           ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG 247
                                                                                         CTTATTGACGATACAAGCGGTGAAGTTCTAGATGAACTGTACCAATTGACGAGGGAGTAC
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                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="TEgg053008"
/clone_lib="XGC-egg"
/dev_stage="egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
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76.1%;
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Pred. No. 3.9e-78;
0; Mismatches 139
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JOURNAL
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                                                                                                  RS Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Fahey, J., Helton, E., Ketteman, M., Madan, J. W., Green, E.D.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671
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                      Klein, S. and Gerhard, D.S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein,S.L., Strausberg,R.L., Wagner,L., Pontius,J.,
and Richardson,P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus laevis (African clawed frog)
  Submitted (07-JUN-2004) National
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTCAGATTGTGAATTTTTGGCCTGCCTTGTATAATCCTTTTTGGGAATTTTTAAACCCCAC
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                                                                (bases 1 to 1193)
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mRNA (cDNA clone MGC:80354
  Institutes of Health, Xenopus
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The NIH Xenopus Clifton, S.W.

VRT 03-AUG-2004

547 610 550

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Best Local :
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     309
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                                                                                                                                            128 TTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTAC
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                                                                                                                                                                                                                                                                                                                          11 CCGGCGCCGTCGCCGACTCCCTCCGATGGCCACAGATGTCTTTAATTTCCAAAAAACCTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gc.series: IRAK Plate: 152 Row: j Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutser, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Likim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mori Teika Olson, Diana Palnquist, Anca Petrescu, Anna Lisa Prabbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: Dr. Igor Dawid cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BC Cancer Agency, Vancouver, BC, Canada info@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project
Contact: XGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development, 610
20892-7510, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                             ACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAG
                                                                                                                                                                                            GTACAAGCCCAGAAGAATTCTTGGCAAGATGGCTTCATCTAAATACATAGCAACGTCC
                                                                                                                                                                                                                                         GTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG---TGTCCAAATCCATCGCCACCACC
                                                                                                                                                                                                                                                                                         CCCGCCCCAGGTGCCGCTGAGCCAATGGCAACCGATATCTTCAATTCCAAAAAACCTGGCT 188
  ACCCAGAACAAGAAGGATGCCGAGAAAATCACAAAGAACCTCATCAAAACAGTCATCAAG
                                                                                               CTGATTGATGATACAAGTGGCGAAGTTCTAGATGAACTCTACCAAGTGACTAGGGAGTAC
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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/protein_id="AAH72904.1"
/db_xref="GI:49115086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clōne="MGC:80354 IMAGE:5074412"
/cissue_type="Ovary, Xenopus"
/clone_lib="WICHD_XGC_Ov1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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|mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 354; DB 5;
Pred. No. 9.7e-78;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 140;
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AUTHORS
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Query Match
Best Local Similarity
Matches 304; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens head and neck tumor and metastasis related mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 515)

Kumar, D., Whiteside, T.L. and Kasid, U.
Identification of a novel tumor necrosis factor-alpha-inducible gene, SCC-22, containing the consensus sequence of a death effects domain of fas-associated death domain-like interleukin-
                                                                                                                                                                                                                                                                                                                                          Submitted (14-OCT-1998) Radiation Medicine, Georgetown University, 3970 Reservoir Road NW, Washington, DC 20007, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                          Kumar,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1beta-converting enzyme-inhibitory protein
J. Biol. Chem. 275 (4), 2973-2978 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGCAGTCTTGTACCGAAACAACCAGTTTAACGAGAAGAGATTGGTCTTATGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTCAAATTGTGAATTTTTAGCTGCTCTGTACAATCCCTTTGGACCTTACAAAAAAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTTAAACCCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCATACAGCGCCATCTCACGGCAAAGTCTCACGGACGTGTTAATAACGTGTTTGACCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTAAGAGAAAGGTCCATCAGCTGGCCATGACTGTGGTCAGCTTCTATCAGGTGGAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTTCCATCAGGTGGATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 515)
50.6%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                      and Kasid, U.
                                                                                                                                                                          protein"
                                                                                             translation="mekfkkkkyhqlamtvvsfhqvdytfdrnvlsrllnecremlhqi"
| QrhlTakshgrvnnvfdhfsdceflaalynpfgnfkphlqklcdginkmldeeni"
                                                                                                                                  /protein_id="AAF29435.1"
/db_xref="GI:6851133"
                                                                                                                                                                                        product="head and neck tumor
                                                                                                                                                                                                                             tissue type="head and neck squamous carcinoma" 1...304
                                                                                                                                                                                                                                                                                                       organism≃"Homo sapiens"
                                                                                                                                                                                                            codon_start=2
                                                                                                                                                                                                                                                                     db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                            .515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:6851132
                                                                                                                                                                                                                                                                                   _type="mRNA"
0;
Score 304; DB 9;
Pred. No. 3.1e-65;
0; Mismatches 0;
                                                                                                                                                                                          and metastasis related
                                 Length 515;
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Gaps
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298 GATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCA

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REFERENCE
AUTHORS
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 31
AC118938/c
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                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                                                                     CE 2 (bases 1 to 164258)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Camarata, J., Campopiano, A., Chang, J., Cock, A., Cook, P., PickHugh, W., Gage, D., Galagan, J., Dodge, S., Faro, S., Ferreira, J., Kells, C., LaRocque, K., Lamazares, R., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacChan, P., McKernan, K., Meldrim, J., Menes, C., McClarthy, M., McEwan, P., McKernan, K., Meldrim, J., Menes, C., Nicol, R., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Semann, S., Severy, P., Spencer, B., Schauer, S., Schupback, R., Semann, S., Severy, P., Spencer, B., Schauer, S., Theodore, J., Viel, R., Vo, A., Wilson, B., M., Traylis, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wi, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Blirren B., Nubhaum, C., Lander, E., Abouelleil a. Allen M. Blien, M. Store, C., Lander, F., Abouelleil a. Allen M.
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Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y. Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus, clone RP24-174015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
1 (Dases 1 to 164258)
Birren,B., Nusbaum,C. and Land
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC118938.3 GI:28475940
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC118938 164258 bp DNA linear HTG 24-FEB-2003
Mus musculus clone RP24-174015, WORKING DRAFT SEQUENCE, 8 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jnpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTT 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGAAGAAACAT 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                         Choepel, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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                                                                                                                                                                                                                                                                              FEATURES
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                                                            misc_feature
                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-FBB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 24, 2003 this sequence version replaced gi:28261544. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 0.960731
Consensus quality: 162606 bases at least Q40
Consensus quality: 162965 bases at least Q30
Consensus quality: 163183 bases at least Q20
Insert size: 164000; agarose-fp
Insert size: 163558; sum-of-contigs
Quality coverage: 11.0 in Q20 bases; sum-of-cont
                                                                                                                                                                                                                                                                                                                                        104530
104630
115027
115127
131678
131778
131778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L25165
Center clone name: 174 0 15
Center clone name: Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37690
37790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29708
29808
32341
32441
clone_end:SP6
                            /note="assembly_fragment
                                                                  /clone_lib="RPCI-24 Male Mouse
1. .29707
                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP24-174015"
                                                                                                                                                                                                                                                                           Location
                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                              104629: gap of 100 bp
115026: contig of 10397 bp in length
115126: gap of 100 bp
131677: contig of 16551 bp in length
131777: gap of 100 bp
158793: contig of 27016 bp in length
158893: gap of 100 bp
164258: contig of 5365 bp in length.
                                                                                                                                                                                                                                                  .164258
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32340:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37789: gap of 100 bp
.04529: contig of 66740 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32440: gap of 100 bp
37689: contig of 5249 bp in length
                                                                                                                                                                                                                                                                              'Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of 100 bp
contig of 2533 bp in length
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375; Conserv
                                                                                                    AC107848
Mus musculus chromosome 9 CLOHE ...
TO DECCRESS ***, 8 unordered pieces.
           AC107848.5 GI:45598920
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
Mus musculus (house mouse)
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158894. .164258
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131778. .158793
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104630. .115026
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32441. .37689
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[15127. .131677
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0; Mismatches 196;
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.9 map 9,
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RS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Bastien, V., Bloom, T., Boyuslavkiy, L., Boukhgalter, B., Cammarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J., Serickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Liu, A., Mabbitt, R., MacLean, C., Kamat, A., Karatas, A., Kells, C., Liu, A., Mabbitt, R., MacLean, C., MacCarthy, M., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacConald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacConald, P., Major, J., Mhova, T., Mlenga, V., Murphy T., Naylor, J., MacCarthy, M., Stojanovic, N., Stubs, M., Stojanovic, N., Stubs, M., Stubs, M., Stojanovic, N., Stubs, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (22-MAR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 22, 2004 this sequence version replaced g1:44886703. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 195574)
                                                                                                                                                   Center project name: L20615
Center clone name: 321_A_19
                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
------Project Information
Center project name: L20615
                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center Center code: WIBR
                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                      -- Genome Center
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me 9, clone RP23-321A19
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civ,L., Boukhgalter,B.,
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FEATURES
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Matches 375;
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CAACAAAATGTTGGATGAAGAGAACATATGA
                                                                                                                                                                                                                                                            CAGGCTGTTAAATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGC
                                                                                                                                                                                                                                                                                                                              TGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATC
                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGATCATGAAGGATGCTATCAAGGTGGCAATCAAAATTGGCATTCTCTACCGGAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                CAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTTCAGATTGTGAATTTTTTGGC
                                                                                                                                                                                                                      TAAGCTTCTGCATGAGTGCAAGGACCTGGTACATGAACTGGTACAGCGACACTTGACACC
                                                                                                                                                                                                                                                                                                     TGCGATGACCATGGTCAGCTTCTACGAAGTAGAGTATACCTTTGATACGAATGTGCTCTC
                                                                                                                                                                                                                                                                                                                                                                                  ACAGTTCAGTCAAGAGGAGGTTATAATTGTGGAGAAAACTCCGGAAGAAACTGAACCAGAC 160288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATCTTTGATGAGCTGTACAAAGTCACAGAAATACACACCCACAACAAGAAGGAGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACAAGTAGTGA
                                                                                                    TGCCTTGTATAATCCTTTTGGGAATTTTAAAACCCCACTTACAAAAACTATGTGATGGTAT
                                                                                                                                       CAGAACCCATGGACGCATAAACCATGTCTTCAACCACTTTGCTGATGTGGAATTCCTTTC
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142784
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7979
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="RP23-321A19"
/clone_lib="RPCI-23 Female Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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30: gap of 100 bp
38: contig of 31158 hm
8: gap of 100 bp
8: gap of 100 bp
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s: gap of 100 bp
s: gap of 100 bp
s: contig of 2478 bp in length
s: contig of 39049 bp in length
s: contig of 39049 bp in length
s: gap of 1100 bp
s: contig of 11480 bp in length
s: gap of 100 bp
s: gap of 100 bp
s: contig of 41211 bp in length
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Pred. No. 1.7e-53;
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                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNI at: http://image.llnl.gov Series: IRAK Plate: 101 Row: c Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 41056158
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
cDNA Library Preparation: Dr. Sumio Sugano and Dr. Ko-ichi Kawakami
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.eystemsbiology.org
contact: amadan@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (23-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci.
12477932
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3986 bp mRNA linear VRT 1
Danio rerio tumor necrosis factor, alpha-induced protein
(cDNA clone MGC:55331 IMAGE:2601021), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anup Madan, Jessića Fahey, Erin Helton, Mark Ketteman, Anura
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 3986)
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/db_xref="taxon:7955"
/clone="MGC:55331 IMAGE:2601021"
/rissue_type="Whole body, adult,
including unfertilized eggs)"
/clone_lib="Sugano Kawakami zebza
                                                                                                                                                                                       strain="AB"
                                                                                                                                                                                                                 organism="Danio rerio"
/mol_type="mRNA"
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/protein id="AAH52765.1"
/db xref="GI:31127058"
/db xref="LocusID:39303"
/db xref="LocusID:39303"
/db xref="HocusID:39303"
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/translation="MDSFSTKNLALQAQKKLMSKMATKTVANLFIDDTSSEVLDELYR
VTKEYTRNRKEAQKIIKNLIKOVEKLHQAINRHLTAKSHARINHVFNHFADCDFLATLY
SFYQIIFTFDRRVMSNLLNDCRELLHQAINRHLTAKSHARINHVFNHFADCDFLATLY
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/note="Vector: pME18S-FL3"
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/db_xref="LocusID:393303"
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Query Match
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                               69467 GATGGCGACCAAGACAGTGGCCAACCTCTTTATAGACGACACCAGCAGCGCGAGGTACTGGA
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220 CAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAA 279
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Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the WORMPEP database can be found at the WORMPEP clone-derived active ac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 205949)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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is from a Zebrafish BAC library
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/db_xref="taxon:7955"
/clone="DKEY-49M19"
/clone_lib="DanioKey"
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                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-NOV-1999) DNA Sequencing and Technology Center,
Submitted (University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                  Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 188937)

Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
                                                                                                                                                                                                                                                           Center
                                                                                                                                                                                                                                                                                                            On Jan 21, 2000 this sequence version replaced gi:6223629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188937 bp
Homo sapiens chromosome 15 clone
SEQUENCE, 10 unordered pieces.
AC015679
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Unpublished
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CAATGACTGCCGTGAACTTCTGCACCAGGCCATCAATCGGCATCTAACGGCGAAATCTCA 69108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTGTTAGCTTCTACCAGATCGACTTCACTTTTGATCGACGCGTCATGAGTAATCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCCCGAATCAACCATGTCTTCAATCATTTCGCCGATTGTGACTTCCTCGCGACGCTATA 69048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 188937)
                                                                                                                                                                                                  Web site: http://sequence-www.stanford.edu/group/human/Contact: hum-info@sequence.stanford.edu
                                                                                                                                                                                                                                                                        Center: Stanford DNA Sequencing
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                                                                                                                                                                                                                                        Center code: SDSTDC
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Best Local Similarity
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                                                                                                                                                                                                                                    51861 CAAGATCATGAAAGACTTAATCAAGGTGGCGATCAAAATCGGGATCCTCTACCGGAACAA
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                                                                                                                                                                                      211 GAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert size: 185828; agarose-fp
Insert size: 188487; sum-of-contigs
Quality coverage: 5.3 in Q20 bases; sum-of-contigs.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374;
                    CAATCTCCTGCATGAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCC
                                                 CAGGCTGTTAAATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGC
                                                                                                                           TGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATC
                                                                                                                                                             CCAGTTTAGCCAAGAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGAC 51980
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2221
7219
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/chromosome="15"
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/clone_lib="RPCI human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
/mol_type="genomic DNA"
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.88937: contig of 49929
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8: gap of unknown length
6: f 49929 bp in
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Pred. No. 4.
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unknown length
g of 14873 bp in i
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On Fe
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Submitted (23-FEB-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, Nesbitt, R., Traicoff, R. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-JUL-2000) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nesbitt, R., Shaffer, T. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Mad Nesbitt, R., Traicoff, R. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC073964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                   AC012169 [drafting
                                                                                                                                                                                                                                                    Sequencing vector: pUC18; L08752
Chemistry: Dye-terminator Big Dye; 90% of reads
Chemistry: Dye-primer Big Dye; 10% of reads
Assembly program: Phrap; version 0.990399
                                                                                                                                                                                                                                                                                                                        Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen0systemsbiology.org
Drafting center: SDSTDC
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                Center: Multimegabase Sequencing Center Center code: UWMSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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/map="15q21.2"
/clone="RP11-394B5"
/clone_lib="RPCI human BAC library 11"
/note="Data from overlapping BACs RP11-105D1
                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                 1. .189796
                                                                                                                                                              ocation/Qualifiers
                                                                           chromosome="15"
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                                                                                          RESULT 37
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Sequence 22:
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                                                     1248 bp DNA
22590 from Patent WO02068579.
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67852 CAATAAGTTGCTAGATGAGAAAGTCCTTTAA 67822
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                                                                                                                                          511 TGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTAT
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                                                                                                                                                                                                                              CAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTTGTGAATTTTTGGC
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                                              CAACAAATGTTGGATGAAGAGAACATATGA
                                                                                                CACCCTCTATAGTCTGGATGGAGACTGTAGGCCCAACCTCAAGAGGATTTGTGAAGGAAT
                                                                                                                                                                                           CAGGACCCACGGGCGTCAACCACGTCTTTAACCACTTTGCCGATGTGGAGTTCCTCTC
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17935. 17940
/note="low quality data"
55786. .56417
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105973. .189796
/note="Overlap with RP11-522G20
161495. .161500
/note="low quality data"
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104690. .104715
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Pred. No. 4.2e-53;
0; Mismatches 197;
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Sequence
CQ841622
                Homo
Homo
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Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                  CQ841622.1 GI:50893409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: WO 02068579-A 22590 06-SEP-2002; PE Corporation (NY) (US)
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Mammalia; Eutheria;
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                sapiens
                         sapiens (human)
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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1. .1248
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Pred. No. 8.2e-53;
0; Mismatches 191;
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Ota, T.,
                                                                                               similar to
AK123281
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 Nakagawa, S.,
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522 ATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGT
                                                                                                                                                                                             AK123281 1986 bp mRNA linear Homo sapiens cDNA FLJ41287 fis, clone BRAMY2038484, similar to Homo sapiens MDC-3.13 isoform 2 mRNA.
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                      AK123281.1 GI:34528784
oligo capping; fis (full insert
Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, J., Isono, Y., Nagai, K. and Iri
Full-length human cdna
Patent: EP 1440981-A 269 28-JUL-2004;
Research Association for Biotechnology
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/mol_type="unassigned DN:
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.3%;
  Senoh, A.,
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Pred. No. 8.3e-53;
0; Mismatches 191
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Mizuguchi, H.,
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Inagaki, H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-JUL-2003) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatrari, Kisarazu, Chiba 292-0818, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Makamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Location/Qualifiers
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ATGAGTGCAAGGACCTGGTGCATGAACTGGTGCAGGGCACCTGACGCCCAGGACCCACG
                                    ATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCCACCTCACTGCCAAGTCACATG
                                                                                                TTGTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGC
                                                                                                                                      TGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTAA
                                                                                                                                                                                                AAGAGGAGCTGGTTATTGTGGAGAAGTTCCGGAAGAAGCTGAACCAGACCGCCATGACCA
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/db_xref="GI:34528785"
/db_xref="GI:34528785"
/translation="MDSDSGEQSEGEPVTAAGPDVFSSKSLALQAQKKILSKIASKTV
/translation="MDSDSGEQSEGEPVTAAGPDVFSSKSLALQAQKKILSKIASKTV
ANMLIDDTSSEIPDELYKVTKEHTHNKKEAHKLMKDLIKVAIKIGILYRNNQFSQEEL
VIVEKFRKKLNQTAMTIVSFYEVEYTFDRNVLSNILHECKDLVHELVQRHLTPRTHGR
INHVFNHFADVEFLSTLYSLDGDCRPNLKRICEGINKLLDEKVL"
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/clone_lib="BRAMY2"
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Pred. No. 8.3e-53;
0; Mismatches 191
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Best Local Similarity Matches 367; Conserv

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Query Match

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JOURNAL REFERENCE
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ACCESSION
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AJ720336
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Gallus gallus mRNA for hypothetical protein,
AJ720336 GI:53133331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fiedler,P., Kutter,S., Blagodatski,A., Kostovska,D., Koter Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M. Full-length cDNAs from bursal lymphocytes to facilitate ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caldwell, R.B., Kierzek, A.M., Arakawa, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Institut fuer Molekulare Strahlenbiologie, Ingolstaedter Landstr.
1, D-85764 Neuherberg, GERMANY
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function analysis
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                                                                                                                         /codon_start=1
/product="hypothetical protein"
/protein_id="CAG31995.1"
/protein_id="CAG31995.1"
/db_xref="GI:5313332"
/tranelation="MDTFSTKMLALQAOKKILSKMASKTVANVFIDDTSSEILDELYR
ATKEYTHNRKEAQKIIKNLIKIVMKLGVLYRNGQFSPEELLVMERFRKKVHTLAMTAV
SFHQIDFTFDRRVVSSVLTECROLLHQAVSSHLTAKSHSRINHVFNHFADYEFLSALY
GPAEFYRTHLKRICEGVNKMLEEDNI"
                                                                                                                                                                                                                                                                                                                  /iocus_ta
141. .701
                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="2 weeks
l. .1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="CB"
                                                                                                              702. .>1589
                                                                                                                                                                                                                                                                            note="ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                         cell_type="lymphocyte"/
tissue_type="bursa"
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                                                                                           locus_tag="RCJMB04_15i14"
                                                                                                                                                                                                                                                                                       locus_tag="RCJMB04_15i14"
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                 42.0%;
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                                                                                                                                                                                                                                                                                                                             tag="RCJMB04_15i14"
Score 252.4; DB 5;
Pred. No. 2.6e-52;
0; Mismatches 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bezzubov, Y.,
                                    Length 1589;
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Fragment Name
AC115187 0
AC115187 1
AC115187 2
AC115187 3
AC115187 3
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Best Local S
Matches 372
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                                                                                                        AGAT CCT GAG CAAGAT AGC CAAAAA CTGT GG C CAA CATGCT GAT CGAT GA CACCAG CA
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CCCACAAGATCATGAAGGATGTAATAAAGGTGGCGATCAAAATTGGTATTCTCTACCGGA
                           CAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGA
                                                                                                                               AGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTA
                                                                                                                                                             CTTTACCCATAGGTCCTCATGTGTTTAGCTCCAAGAGTCTCGCCCCTTCAAGCCCCAGAAGA
                                                                                                                                                                                       CTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGAAGAGAACATATGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGA 463
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                                                                           GTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTACCGAGCCACGAAGGAGTACACTCACAATCGCAAAGAGGCCCCAGAAGATCATCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACACCTTCAGCACCAAGAACTTGGCCCTGCAGGCCCAGAAGAAGCTCTTGAGCAAAATG
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64.7%;
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AUTHORS
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AC115505/c
LOCUS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACI15505.4 GI:2518846/
HTG; HTGS_PHASE1; HTGS_DRA
Rattus norvegicus (Norway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC115505 256285 bp | Rattus norvegicus clone CH230-77C4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
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HASE1; HTGS_DRAFT; HTGS_
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GTATCAACAAAATGTTGGATGAAGAGAACATATGA 601
GAATCAATAAATTGTTAGATGACAAAATCCTCTGA 32313
                                                                                                                                                                     TTTCCACTCTCTACAGTCCGCACGGAAACTGCAGGCCCAATCTCAAGAGGATTTGCGAAG 32348
                                                                                                                                                                                                                                                                                                                                      CGCCCAGAACCCACGGACGCATAAACCATGTCTTCAACCACTTCGCTGATGTGGAATTCC 32408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTCTAAACTTCTGCATGAGTGCAAGGACCTGGTCCATGAACTGGTACAGCGACACTTGA
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                                                                                                                                                                                                                                                   TGGCTGCCTTGTATAATCCTTTTGGGAATTTTTAAACCCCACTTACAAAAACTATGTGATG 566
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; _ENRICHED DNA linear HTG 23-NOV-, *** SEQUENCING IN PROGRESS

Pasternak,S., Paul,... Pasternak,S., Poindexter,A., Popovic, D., Primus, E.,

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                                                                                                                                                                                     and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 23, 2002 this sequence version replaced gi:23269911. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 256285)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genoshotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                           as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: GSWY
Center clone name: CH230-77C4
Center clone name: CH230-77C4
Center clone name: CH230-77C4
Center clone name: CH230-77C4
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 199255 bases at least Q40
Consensus quality: 203424 bases at least Q30
Consensus quality: 203424 bases at least Q20
Consensus quality: 206379 bases at least Q20
Estimated insert size: 195822; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
     24558
24658
201811
201911
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     201810:
201910:
214313:
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24557: contig of 24557 bp in length 24657: gap of unknown length 201810: contig of 177153 bp in length 201910: gap of unknown length 214313: contig of 12403 bp in length
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GTATCAACAAAATGTTGGATGAAGAGAACATATGA 601
                                                       TTTCCACTCTACAGTCCGCACGGAAACTGCAGGCCCAATCTCAAGAGGATTTGCGAAG 120073
                                                                                               TGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATG
                                                                                                                                             CGCCCAGAACCCACGGACGCATAAACCATGTCTTCAACCACTTCGCTGATGTGGAATTCC 120133
                                                                                                                                                                                       CTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTT
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228541. .229886
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                                                                      JOURNAL
                                                                                                                                                                                                                                      Muzny, Diazle, Mariker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Allen, H., Alsbrooks, S., Allen, H., Alsbrooks, S., Allen, H., Barder, M., Barnstead, M., Benahmed, F., Barder, M., Barder, M., Barnstead, M., Benahmed, F., Barder, M., Barder, M., Barnstead, M., Berom, B., Cardenas, V., Carter, K., Cavazos, I., Cesasr, H., Center, A., Cher, A., Drobe, M., Craber, D., Davila, M., L., Davis, C., Dor, C., Coyle, M., Cree, A., D., Souza, L., Davila, M., L., Davis, C., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, A., Begene, C., Bvans, C.A., Falls, T., Fan, G., Detertch, D., Dergano, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan, A., Begene, C., Bvans, C.A., Falls, T., Fan, G., Perandrez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, S., Finley, M., Falgy, M., Forbee, L., Foster, M., Gebregeovgis, B., Geor, K., Gill, R., Garcia, A., Garrer, M., Gebreara, W., Ghararde, P., Haaland, W., Hamilton, C., Lond, C., Hamilton, C., Lond, C., Hamilton, C., H
Submitted (30-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
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Rattus norvegicus clone CH230-112K14,
                                                                                                                                                                                          Unpublished
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC129440.3
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                                 ORIGIN
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REFERENCE
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On May 13, 2003 this sequence version replaced gi:23264293.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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266730
266830
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Center clone name: CH230-112K14

Center clone name: CH230-112K14

Center clone name: CH230-112K14

Center Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 224959 bases at least Q40

Consensus quality: 227786 bases at least Q30

Consensus quality: 2279294 bases at least Q30

Consensus quality: 229294 bases at least Q30

Estimated insert size: 236137; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                               268870
268970
270128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: hgsc-help@bcm.tmc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.hgsc.bcm.tmc.edu/
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                           end_sequence:BH258362"
                                                                                                                                                                        complement (4198.
                                                                                                                                                                                          /db xref="taxon:10116"
/clone="CH230-112K14"
                                                                                                                              /note="clone_boundary
/note="wgs_contig"
                                                                                                                                                                                                                                                                                    organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                             ocation,
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contig of 2040 bp in length
gap of unknown length
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gap of unknown length
contig of 260184 bp in lengt
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bp in length.
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length
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                                                                                                         AUTHORS
                                                                                                                                                       JOURNAL
                                                                                                                                                                                           TITLE
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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausmer, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G. Altschul, S. F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K. Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
                                                                                                                                                       initiative
Dev. Dyn. :
                                                                                                                                                                                                                                                                                                                                                                                              BC076797 1938 bp
Xenopus laevis MGC83729 protein,
IMAGE:6639647), complete cds.
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                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                    (bases 1 to 1938)
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                                                                                                                                                                                                           Richardson, P
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                                                                                                                                                                                                                        S.L., Strausberg, R.L., Wagner, L.,
                                                                                                                                                                                       and genomic tools for Xenopus
                                                                                                                                                       225 (4), 384-391 (2002)
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                                                                                                                                                                                                                                                                                                                             frog)
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                                                                                                                                                                                                                                                                          Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                                                                                                                         Clifton, S.W
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PUBMED
REFERENCE
AUTHORS
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COMMENT
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 Query Match
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Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Generation and initial analysis of more than 15,000 full-length
human and mouse of DNA securation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 158 Row: d Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy L Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Mor Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-JUL-2004) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project
Contact: XGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein, S. and Gerhard, D.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into@bcgsc.bc.ca
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RVFNHFADVEFLTALYSLEGNYRPYLKRICEGVNKLLDERVL"
                             /translation="MDTDSGDLSEGELSPGPEQFSSKSFAVQAQKKILSKMATKTMAN
MLIDDTSSEIFDELFKVTKEYVKNKKEAHKVLKDLVKVAVKVGILYRNKQFSLEELEI
VENFRKKLNQTCMTAVSFFEVEYTFDKNVLSGLLHECKTLLHELVQRHLTPKSHSRID
                                                                                                                                     /product="MGC83729 protein"
/protein_id="AAH76797.1"
/db_xref="GI:49899743"
/db_xref="LocusID:446389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    /gene="MGC83729"
                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MGC83729"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                       db_xref="LocusID:446389"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                  codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="MGC:83729 IMAGE:6639647"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sue_type="Oocytes"
ne_lib="NICHD_XGC_OO1"
host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pCMV-SPORT6.1"
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38.5%;

Score

231.2;

DB 5;

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RESULT 45
BC053167
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     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
            RS Strausberg, R.L., Peingold, B.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Generation and initial analysis of more than 15,000 full-length
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BC053167
BC053167.1 GI:31418810
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Generation and initial analysis of more than 15,000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GACAGGGTTTTTAATCATTTTGCTGATGTGGAATTCCTTACTGCCCTCTATAGCCTTGAA 630
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  224 AACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAA
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This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Leonard I. Zon, M.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad.
12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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(bases 1 to 1813)
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HVFNHFADVDFLTELYGPSEDYRLNLRKICDGINKLLDEGTL"
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(protein id="AAH53167.1"
(db_xref="GI:31418811"
(db_xref="GI:31418811"
(db_xref="GI:3193322"
(db_xref="MDSDSGEQSEGELSPGHESFNSKSLALQAQKKILSKMATMAVAN
/translation="MDSDSGEQSEGELSPGHESFNSKSLALQAQKKILSKMATMAVAN
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/db_xref="LocusID:393322"
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/tissue_type="Kidney, zebrafish"
/clone_lib="NCI_CGAP_ZKid1"
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No. 1.5e-45;
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Search completed: July 28, 2005, 18:12:59 Job time: 3108 secs
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                                                                                                                                                                                                                                         649 CGGATTGACCACGTTTTCAACCATTTCGCCGATGTGGATTTCCTGACCGAGCTGTACGGC 708
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Ada56241 Gene enco
Ash14888 Human cDN
Ash14793 Human cDN
Ash14793 Human cDN
Adr14214 Human NF-
Adr14216 Human mRN
Adr14216 Human mRN
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Adar6332 Cotton cD
Adp98647 C. albica
Ada49996 Wheat gen
Ada79611 Human mus
Aba20411 Human nov
Abx60109 CDNA encoo
Adj30859 Human nov
Abx60109 CDNA encoo
Adj30859 Human mus
Abk91542 Modified
Aak91541 Modified
Aak91549 DNA encoo
Adj30879 DNA encoo
Adj30879 Human bre
Acn79790 Breast ca
Acn8663 Breast ca
Acn8663 Breast ca
Acn8668 Breast ca
Acn86689 Human tum
Adq79906 Rat MURR1
Add60089 Mouse hom
Add13931 Wheat ser
Adj6936 Human mus
Abg8986 Human mus
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Abk34943 Human CDN
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Aaf59594 Human cel
Ach76016 Human gen
Aac10352 Human gen
Aac10352 Human sec
Abl07183 Drosophil
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Abl07182 Drosophil
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Ach68751 Human cDN
Aah18715 Human cDN
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                                                                                         The invention relates to an anti-apoptopic gene SSC-S2 and encoded protein. The gene is a positive mediator of tumour growth and metastasis in certain cancer types. The SSC-S2 protein can be expressed by standard recombinant methodology. The SSC-S2 polypeptide is useful as a target for identifying compounds that modulate cancer progression by inhibiting apoptosis, as a target for detecting cancers where this polypeptide is overexpressed, e.g. renal and ovarian cancers, and leukemia. The antibody and antisense oligonucleotide can be used to treat cancer and to inhibit cancer cell proliferation and/or metastasis. The present sequence represents a human SSC-S2 protein encoding cDNA
                                                                                                                                                                                                         Claim 2;
                                                                                                                                                                                                                                   New SCC-S2 polypeptides and nucleic acids encoding them, useful autarget for identifying compounds that modulate cancer progression inhibiting apoptosis, as a target for detecting cancers, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSC-S2; apoptosis;
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                                  03-OCT-2001;
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The invention relates to a novel method for identifying a compound that CC modulates T lymphocyte activation. The method comprises contacting a T CC cell comprising an A-raf-1 or TCPTP/PTPN2 polypeptide with a compound, CC where the A-raf-1 or TCPTP/PTPN2 polypeptide is encoded by a nucleic acid that hybridises to a nucleic acid encoding a polypeptide having a CC sequence selected from two 606-amino acid sequence and a 415-amino acid sequence given in the specification. The method of the invention has CC immunosuppressive, antiasthmatic, antiallergic, and antiinflammatory CC activity. The method is useful for identifying compounds that modulate CI lymphocyte activation and migration, and for monitoring changes in cell Surface marker expression, cytokine production, antibody production, CC proliferation and differentiation, and apoptosis, using either cell lines CC corp rimary cells. The A-raf-1 or TCPTP/PTPN2 proteins may be used as CC drug targets for compounds that suppress or activate lymphocyte activation and migration, e.g. for the treatment of diseases in which CC modulation of the immune response is desired such as delayed type CC and acute and chronic inflammation. Modulators of lymphocyte activation and care useful for treating disorders related T and B cell activation and CC invention.
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AAX97916 to AAX98029 represent 110 isolated human secreted protein genes. AAY36224 to AAX36727 represent the secreted proteins encoded by the 110 human genes. The genes and their corresponding secreted polypeptides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 110 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or

New isolated human genes encoding secreted polypeptides

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                                                                   cancer; inflammation; immune disorder; neurological disorder;
blood clotting disorder; food additive; food preservative;
storage capability; fat content; nutritional component; ds; gene;
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continuous relates to an isolated HKABT24 nucleic acid molecule. The polypeptides, nucleic acids and antibodies are useful for diagnosing a compathological condition or a susceptibility to a pathological condition, components, treating, or ameliorating a medical condition, such as concer, inflammation and other immune disorders, neurological and blood clotting disorders. The nucleic acids are also useful for chromosome condition, radiation hybrid mapping or long-range restriction companing. The polypeptides and antibodies are useful for providing companing. The polypeptides and antibodies are useful for providing components for differential identification of the tissues communohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to concrease or decrease storage capabilities, fat content or other convert human secreted protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic sendate. Unance of the printed specification but was obtained in electronic conditions.
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                                       GCCGTTCANGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACC
                                                      GCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACC
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                                                                                                                                                    Conservative
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New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or
                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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neurodegenerative disorders

SEQ ID NO 430; 1754pp; English.

CC neurodegenerative disorders, or polypeptides comprising an amino acid CC sequence at least 95% identical to the new sequences. The polypeptides, and the controlled controlled controlled the polypeptides, agonists or antagonists that binds to the polypeptide, are useful in preparing diagnostic or pharmaceutical compositions for diagnosing, treating or preventing an e.g. immune CC disorders, inflammatory conditions (e.g. inflammatory bowel disease, ce phritis or Crohn's disease), respiratory disorders (e.g. asthma and CC enghritis or Crohn's disease), respiratory disorders (e.g. asthma and CC enghritis or crohn's disease), respiratory disorders (e.g. asthma and CC enghritis or controlling gene or Alzheimer's disease), and CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The CC polynucleotides are useful for chromosome identification, chromosome CC mapping, for controlling gene expression through triple helix formation or antisense DNA or RNA, in gene therasp, for identifying individuals CC from minute biological samples, in forensic biology, and as hybridization controlling neural disorders (e.g. els, to raise antibodies, for testing biological activities, and for treating or preventing neural disorders, immune system disorders, creating or preventing neural disorders, immune system disorders, and for the sequence data for this patent did form part of the printed specification, but was obtained in electronic format directly from WIPO at first enumerces. The invention relates to 592 new human secreted polypeptides useful fo diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or ftp.wipo.int/pub/published_pct_sequences.

Sequence 1943 BP; 629 A; 325 C; 399 G; 586 T; 0 U; 4 Other;

Query Match Best Local (Matches Local 590; h 97.9%; Similarity 99.3%; Conservative ٥, Score 588.2; DB 10 Pred. No. 1.4e-163; Mismatches DB 10; Indels Length 1943 0 Gaps

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                                                                        CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC complementary strand of a polynucleotide comprises or (b) a combination
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a 5'-end
CC complementary strand of a polynucleotide which comprises a function of
CC complementary strand of a polynucleotide which complementary to a
CC polynucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC constant of the primers are useful for synthesising polynucleotides,
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC chast seasily without any specialised methods. AAH03166 to AAH13628 and
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH3672 represent human acdid sequences; AAB92446 to AAH3628 and
CC consent invention
CC cresent invention
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
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length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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 29-JUL-1999;
27-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Primer sets for synthesizing polynucleotides, particularly the 5602 full-
length cDNAs defined in the specification, and for the detection and/or
diagnosis of the abnormality of the proteins encoded by the full-length
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length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dr primer and an oligonucleotide complementary to the
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, Sugiyama T, Wakama
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                                                                                                                                      TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGC
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TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                 TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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99.8%;
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A, Nagai K,
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This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antiirheumatic, gastrointestinal-Gen, antiasthmatic, antiarthritic, antirheumatic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides useful for diagnosing, preventing, treating, or ameliorating conditio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disorder; NF kappaB regulation; cancer; aberrant apop hepatic disorder; Hodgkin's lymphona; haematopoietic tumour; hyper-IgM syndrome; hypohidrotic ectodermal dysplasia; X-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; inf viral replication; host cell survival, evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotides and polypeptides associated with pathway, useful for diagnosing, treating, or preventing disorc diseases associated with NF-kappaB pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; aberrant acute phase response, recongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer; HIV propagation; gene; ds; human.
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cc immune diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder crelated to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, chepatic disorders Hodgkin's lymphomas, haematoppietic timours, hyper-IgM cc syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic cc ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, cc hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell cc survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick cc syndrome, stroke, EAB, autoimmune disorders, disorders related to hyper cc immune activity, disorders related to aberrant acute phase responses, cc hypercongenital conditions, birth defects, necrotic lesions, wounds, corgan transplant rejection, conditions related to organ transplant cc rejection, disorders related to aberrant signal transduction, disorders related to aberrant signal transduction, conditions related to organ transplant cc proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the invertion where the sequence is that of a human gene which is incompanied to invertion where the sequence is that the sequence is continued to invertical the sequence is that of a human gene which is invertical to the novel association with the NF-kappaB pathway of the invertical to the novel association with the NF-kappaB pathway of the sequence is t
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X-linked anhidrotic ectodermal dysplasia; immunodeficiency;
viral infection; HIV-1; HTIV-1; hepatitis B; hepatitis C; EBV; influenza
viral replication; host cell survival; evasion of immune response;
rheumatoid arthritis; inflammatory bowel disease; colitis; asthma;
atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
autoimmune disorder; hyper immune activity;
aberrant acute phase response; hypercongenital condition; birth defect;
necrotic lesion; wound; organ transplant rejection;
aberrant signal transduction; proliferating disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to the novel association of protein sequences the genes which encode them) to the NF-kappaB pathway. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 217; 237pp; English.
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12-MAY-2003; 2003US-0469757P
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inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;
hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;
subject to the novel association with the NF-kappaB pathway invention. Note: This sequence does not appear in the specified obtained by the indexer from Genbank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV propagation;
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Best Local Similarity
Matches 565; Conserv
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                                              01-MAR-2002; 2002US-00087192
                                                                    28-FEB-2003; 2003WO-US006235
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                         (SAGR-) SAGRES DISCOVERY
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ilarity 99.8%;
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Recombinant nucleic acid useful for diagnosis and treatment comprises a nucleotide sequence.
                                                                                           2003-328604/31
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                                                                                   carcinoma
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SEQ ID

NO 497; Opp; English.

The present invention relates to novel DNA and protein sequences which CC are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) as a biochip; (cx) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent CX US2002182586A1, for which no sequence data was published

Sequence 2034 BP; 639 A; 352 C; 412 G; 631 Η, 0 U; 0 Other;

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Query Match
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RESULT 11 ADR14038 ID ADR14

ADR14038 standard; DNA; 2081

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CC This invention relates to the novel association of protein sequences (and CC the genes which encode them) to the NF-kappaB pathway. The invention may CC be useful for the production of compounds with an antiinflammatory, CC cytostatic, hepatotropic, virucide, antiarthritic, antiinfumatic, CC gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or conseiul for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder crelated to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic cetodermal dysplasia, X-linked anhidrotic cetodermal dysplasia, Y-linked anhidrotic survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper congenital conditions, birth defects, necrotic lesions, wounds, crejection, disorders related to aberrant signal transglant responses, for the province of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunosuppressive; vulnerary; gene therapy; immune disorder; inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis; hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour; hyper-IgM syndrome; hypehidrotic ectodermal dysplasia; Y-linked anhidrotic ectodermal dysplasia; immunodeficiency; viral infection; HTV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral replication; host cell survival; evasion of immune response; rheumatoid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; enthyroid sick syndrome; stroke; EAB; autoimmune disorder; hyper immune activity; aberrant acute phase response; hypercongenital condition; birth defect; necrotic lesion; wound; organ transplant rejection; aberrant signal transduction; proliferating disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 39; 237pp; English.
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12-MAY-2003; 2003US-0469757P.
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propagation in cells infected is that of a human gene which
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Best Local Similarity
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           01-MAR-2002; 2002US-00087192
                                                                                                                     Cytostatic; carcinoma; lymphoma; cancer; human;
                                                                                                                                           Human genomic sequence hCG36837
                                                                                                                                                                  18-NOV-2004
                                                                                                                                                                                                             ACN44178 standard;
                                28-FEB-2003; 2003WO-US006235.
                                                                           WO2003073826-A2
                                                                                                 Homo sapiens
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma hasociated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
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AAATGTTGGATGAAGAGAACATATGA 47503
                    AAATGTTGGATGAAGAGAACATATGA
                                                                                         TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
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99.8%;
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RESULT 13
                                           sequence and an oligonuclectide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18742 represent human cDNA sequences, AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                   length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer sets for synthesizing polynucleotides, particularly the 5602 ful length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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09-JUN-2000;
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27-AUG-1999;
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Sugiyama T, Wakamatsu
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2000JP-00118776.
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2000JP-00241899.
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C, Otsuki
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                                                 New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alternations or as tools for
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
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Crearesion, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and creating at least 8 amino acids of any of the 6808 amino acid sequences fully defined in the specification. The probe is a single exon probe that the hybridises under high stringency conditions to a nucleic acid molecule cardinates of the specification. The probe is a single exon probe that the hybridises under high stringency conditions to a nucleic acid molecule cardinates to the specification. The probe is a single exon probe that the hybridises under high stringency conditions to a nucleic acid molecule cardinates of the specification. The probe is a single exon probe cardinates of the plurality of probes is separately cardinates of the plurality of probes is separately and addressable set of single exon nucleic acid molecule exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of measuring human gene expression, a method of contiguous amino acids of any of the above- mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing than gene expression data by subscription, and a computer-readable constitution, which contains a database having a plurality of records (each record including data on the expression of a single exon mrocarrays. Created above, methods and apparatus are useful in gene expression, or in contains and attabase of selling exon probe cated as tools for surveying the probes are used in identifying and characterising gross calleration, the probes are used in identifying and characterising gross allerations in the genomic locus that includes their exon, in assessing selling exon probe of the invention. Note: The sequence is a human cardinated in electronic format direc
  Sequence 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 22914; 80pp; English
BP; 175 A; 109 C; 117 G; 143 T; 0 U; 0 Other
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Matches 543; 301 181 361 241 121 156 456 CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT 61 96 GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG TGTTAAATGAATGCAGAGAGGTGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCCACCTCACTGCCAAGT TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTA TTAATCAAGATGAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCCAAAACAAGAAGGAGGGCAGAGAAGA GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG Conservative 0; Mismatches es 1; Indels 0; Gaps 515 30C 180 155 420 455 360 395 335 240 275 215 120 60

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Query Match

Local Similarity

90.2%;

Score 542.4; DB 12; Pred. No. 2.9e-150;

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                                                                                                                                        The present invention relates to novel DNA and protein sequences which care associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (iv) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (vii) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining carcinoma or a propensity to carcinoma; and (xi) for capable of capable on the CAP are useful as DNA vaccines and the CAP are useful as markers of sequence. Note: This patent is an equivalent to basic patent CA coding US2002182586A1, for which no sequence data was published
                                                                                Query Match
Best Local S
Matches 494
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 493; Opp; English.
                                                                                                                                                                                                                                                                                                                                    Recombinant
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GATCCTGGGCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAG
             GATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACGACACAAGTAG
                                                    TCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAA
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RESULT 16
ACN44177
The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
                                                                                                                                                                                                                   Recombinant nucleic acid useful for diagnosis comprises a nucleotide sequence.
                                                                                                                                                                  Claim 1; SEQ ID NO 494; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002; 2002US-00087192
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA gene sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2087 BP; 556 A; 487 C; 508 G; 536 T; 0 U; 0 Other;
   07-FEB-2001
                                   EP1074617-A2
                                                                                                                                                                                                                                            AAH07641 standard;
                                                                                                                                                                          26-JUN-2001
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                                                                    sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                      cDNA clone (5'-primer) SEQ ID NO:4476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGAAGATCTTGG
                                                                                                    primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACATGGACGGGTTAATAATGTCTTTGATCATTTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCATCAAGAACCTCATCAAGACGGTCATCAAGCTGGCCGTCCTCCACAGGAACAATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAAAATGGTATCCAAATCCATCGCCACCACGCTGATCGACGACACCAGCAGCGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                                                                                               AAATGTTGGATGAAGAGAACATATGA 1073
                                                                                                                                                                                                                                                                                                                                                                 AAATGTTGGATGAAGAGAACATATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAATCAAGACGAGCTGGCGCTCATGGAGAAGTTCAAGAAGAAGGTGCACCAGCTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGCTACAGATGTCTTCAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGATTGTGATTTTTTGGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTACCGCCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGACGGTCGTCAGCTTCCACCAGGTAGAGTACACCTTCGACCGCAATGTGCTGTCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                        (first entry)
                                                                                                    detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.9%;
86.6%;
                                                                                                                                                                                                                                            cDNA;
                                                                                                                                                                                                                                            587
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Pred. No. 6.8e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                 601
                                                                                                    antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                   575
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180

GGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG

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TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG

GGGAGTACACCCAAAACAAGAAGGAGGAGGAGAAGATCATCAAGAACCTCATCAAGACAG
TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA

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                                                                                                                                                                                                                                                                         CC length cDNAs defined in the specification. Where a primer set comprises:

(C (a) an oligo-dT primer and an Oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination

CC of an oligonucleotide comprising a sequence complementary to the

CC complementary strand of a polynucleotide which comprises a 5'-end

CC sequence and an oligonucleotide comprising a sequence complementary to a

CC polynucleotide comprises at least 15 nucleotides and the combination of

CC the 5'-end sequence/3'-end sequence is selected from those defined in the

CC polynucleotide number sets can be used in antisense therapy and in

CC place therapy. The primers are useful for synthesising polynucleotides,

CC particularly full-length cDNAs. The primers are also useful for the

CC particularly without any specialised methods. AAH03166 to AAH13628 and

CC DNAs easily without any specialised methods. AAH03166 to AAH13628 and

CC DAH13633 to AAH19742 represent human cDNA sequences; ABB92446 to AAH3632 represent

CC oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                   Query Match
Best Local S
Matches 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer sets for synthesizing polynucleotides, particularly the 5602 fullength cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HELI-) HELIX RES INST.
                                                                                                                                   105
 225
                   120 CCACCACCTTAATAGACGACACAAGTAGTGGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                  165
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                                                                                                    60
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3, Sugiyama
                                                                                                                                                                                                                      Similarity
                                                                                                                                     CTTCAGCGTCCCGGCGCCGTCGCGCCACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                                                                                                                        CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                                                                                                                                                                                                                                         587
 CCACCATTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID
                                                                    AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                      AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-00300253.

2000JP-00118776.

2000JP-00183767.

2000JP-00241899.
                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                       BP; 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishikawa T,
                                                                                                                                                                                                                      65.7%;
96.6%;
                                                                                                                                                                                                                                                                       A; 146 C; 140 G; 116 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               describes primer sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2537pp +
                                                                                                                                                                                                    0
                                                                                                                                                                                                                      Score 394.6; DB 4;
Pred. No. 2.2e-106;
                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for synthesising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K,
Otsuki
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
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                                                                                                                                                                                                    <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5602 full-
                                                                                                                                                                                                    Gaps
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문 S 밁 S 딹

269

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RESULT 18
ADQ63108
ID ADQ63
XX ADQ63
XX ADQ63
XX NOVE
DE NOVE
EX NOVE
EX NOVE
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                                                                                                                                                                                    Query Match
Best Local S
Matches 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, S
Yamamoto J,
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to 2495 novel polynucleotides (I) and their encoded polypeptides, sequences hybridizing to these nucleotides, sequences encoding partial polypeptides and sequences having 70% or 90% identity to the nucleotide and protein sequences. The nucleotides and polypeptides are useful as diagnostic markers or therapeutic target for the diseases or morbid states. They are also useful for treating osteoporosts, neurological diseases, Alzheimer's diseases, Parkinson's diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia;
                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JAN-2003; 2003JP-00102206.
09-MAY-2003; 2003JP-00131392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2004; 2004EP-00001196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-535376/52.
DB; ADQ65296.
                                  102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405
                                                                                                                                    42
                                                                                                                                                                                                            Similarity
TGGTGTCCAAATCCATCGCCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATG
                                                                                                                                                                                                                                                                                                                                      and various cancers. This sequence corresponds to a nucleotide of the invention.
                                                                                                                                                                                                                                                                                      1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; cDNA; 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGNGADATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGNCAGTTTCCAACAAG
                                                                               CTGATGTTTTAGTTCAAAGAGTCTTGCGCTTCAAGCCCAGAAGAAGATTCTGAGCAAAA
                                                                                                                            CAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCACCAAAACANTTA
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J, Isono Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
                                                                                                                                                                                                                                                                                    B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                 536 A; 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269;
                                                                                                                                                                                                    42.38;
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Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2449pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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                                                                                                                                                                                  Score 254.4; I
Pred. No. 1.6e-
0; Mismatches
                                                                                                                                                                                  ٥,
                                                                                                                                                                                                                                                                               C; 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T, Wakamatsu A,
, Irie R;
                                                                                                                                                                                                                                                                                 Ģ
                                                                                                                                                                                                                                                                                    495
                                                                                                                                                                                                         1.6e-64;
                                                                                                                                                                                                                                 DB 12;
                                                                                                                                                                                                                                                                                 T; 0 U;
                                                                                                                                                                                  191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sato
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                    0 Other;
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                                                                                                                                                                                                                                    1986;
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                                                                                                                                                                                  0;
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                                                                                                                                                                                  Gaps
                                                                                                                               101
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                                                                                                  Tang TY, Zhang A
Zhou P, Ghosh M
Haley-Vicente D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic neuroprotective; antianaemic; anticoagulant; thrombolytic; vulnerary; antiulcer; osteopathic; immunosuppressive; antiinflammatory; cytostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; diagnostic; drug screening; forensics; gene mapping; biodiversity assessment; Parkinson's disease; Alzheimer's disease; neurodegenerative diseases; anaemia; platelet disorder; wound;
                                                                                                                                                                                                                                                       24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                         24-SEP-2002;
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                                                                                                                                                                                                       HYSEQ INC
                                                                                                                          Zhang J,
Ghosh M,
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CC ADC3089) and the polypeptides they encode (ADC30890-ADC3080). The Crivention also relates to nucleic acid sequences over 99% identical with Cthe novel human cDNAs. The invention additionally encompasses expression convectors and host cells comprising a nucleic acid of the invention; the crecombinant production of a polypeptide of the invention; an antibody consists a polypeptide of the invention; an antibody constitution further discloses methods of peventing, treating or ameliorating a medical condition; kits comprising polynucleotide probes convention; methods for the invention of compounds that modulate the convention; methods for the polynucleotide probes convention; methods for the polynucleotide and/or monoclonal antibodies for carrying out the methods of the expression or activity of the polynucleotide and/or polypeptide; and 767 contig sequences corresponding to the CDNA sequences of the invention convention for mucleic acids and polypeptides of the invention are constituted in diagnostics, drug screening, forensics, gene mapping, in the contification of mutations responsible for genetic disorders or other creating biodiversity, and in producing many other types of data and products dependent on DNA and amino acid sequences. They are calso used for treating diseases such as Parkinson's diseases or cancer. The nucleic acids may also be used as hybridisation probes or concers, and in the recombinant production of a protein. The polypeptides care also useful in generating antibodies, as molecular weight markers, can and as food supplements. The present sequence represents a specifically collaboration and electronic format directly from WIPO at the sequence data for this patent did not form part of the printed specification, but was considered in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Sim:
Matches 359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 969 BP; 264 A; 261 C; 257 G; 187 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences.
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                                              ATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATG
                                                                                                                                          TTGTCAGCTTCTATGAGGTGGAATACACCTTCGATAGGAACGTGCTCTCCAATCTCCTGC
                                                                                                                                                                                            TGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTAA
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ATGAGTGCAAGGACCTGGTGCATGAACTGGTGCAGCGGCACCTGACGCCCAGGACCCACG
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Pred. No. 2.6
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide concerns in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon mucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon probe cited antibody that binds specifically to a peptide cited above, an isolated antibody that binds specifically to a peptide cited above, and a conjunction of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records
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(RANK/) RANK D R.
(HANZ/) HANZEL D !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human genome-derived single exon nucleic acid probes useful for gene expression analysis, for identifying or characterizing alternate splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 25411; 80pp; English.
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splicing
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ing event; genomic alteration.
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                 Human; NOVX; human disease; NOVX-associated disorder; cancer; addicti Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; str tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome;
                                                                                                                             DNA encoding
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                                                                                                                                                                                                                                                  ABS78741 standard; DNA;
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                                                                                                                             human
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                                                                                                                                                                    (first entry)
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ataxia-telangiectasia;
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Pred. No. 9.1e-60;
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leukodystrophy; anxiety; pain;
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밁 Ś 밁 ঠ 밁 δ 밁 δ 묽 Ś 밁 S 밁 δ 밁 á 밁 S

parasitic

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The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, preferably a NOVX-associated disorder. The NOVX nucleic acids, or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, erebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia-telangicctasia, leukodystrophies, addiction, anxiety, depression, pain, infertiity, inflammatory bowel disease, inflammatory bowel disease, infertiity, inflammatory bowel disease, atherosclerosis, hypertension, sclerosity, inflammatory bowel disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versus-bost disease. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, wound healing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-WAR-2001;
09-MAR-2001;
12-MAR-2001;
13-MAR-2001;
13-MAR-2001;
14-MAR-2001;
20-MAR-2001;
20-MAR-2001;
20-MAR-2001;
21-MAR-2001;
22-MAR-2001;
23-MAR-2001;
26-MAR-2001;
26-MAR-2001;
27-MAR-2001;
28-MAR-2001;
28-MAR-2001;
02-MAR-2001;
02-MAR-2001;
                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                               New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spytek KA, Vernet CA, Tchernev
Li L, Zerhusen BD, Patturajan
Zhong M, Gangolli EA, Taupier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parasitic infection; graft-versus-host disease; cell differentiation; cell proliferation; haematopoiesis; wound healing; angiogenesis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-MAR-2002;
                                                                                                                                                                                                                                                                                                                                Parkinson's disease.
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DB; ABG97497.
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2001US-0274849P

2001US-0275379P

2001US-0275579P

2001US-0275601P

2001US-0277339P

2001US-0277337P

2001US-0277337P

2001US-0277331P

2001US-0277331P

2001US-0277833P

2001US-02778152P

2001US-027894P

2001US-027894P

2001US-027894P

2001US-027894P

2001US-0280802P

2001US-02880802P

2001US-0288148P

2001US-0288148P

2001US-0338375P

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usev VY, Keku
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Pena CEA;
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Matches 347; Conserv
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              antiasthmatic; cardiant; vasotropic; neuroprotective; nootropic; SECP; anticonvulgant; antiparkinsonian; cerebroprotective; antinflammatory; immunosuppressive; human secreted protein; cell proliferative disorder; arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS; allergy; anaemia; asthma; cardiovascular disease; developmental disorder; ischaemic heart disease; congestive heart failure; neurological disorder; renal tubular acidosis; hypothyroidism; Albelmer's disease; dementia;
                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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  Parkinson's
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09-NOV-2000;
16-NOV-2000;
21-NOV-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated human secreted protein (SECP) polypeptide from 63 fully defined protein sequences given in the specification. The polypeptide is useful for the diagnosing/treating of a disease with decreased/overexpression of SECP. Examples of disorders associated with abnormal expression of SECP include a cell proliferative disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory disorder, ALDS, allergies, anaemia, asthma; cardiovascular disease e.g. congestive heart failure, ischaemic heart disease; developmental disorder e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g. Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke. The SECP polymucleotide and polypeptide are further useful for analysing the proteome of a tissue or a cell type. The polymucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or rats) to model human disease, and for somatic or germline gene therapy, and for the polymucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or protein the polymucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or protein the polymucleotide is useful for creating knockin humanised animals (pigs) or transgenic animals (mice or protein the polymucleotide is useful for creating the polymucleotide is useful for creating the protein for analysing the protein for ana
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Sanjanwala M, Thornton
Ding L, Hafalia AJA, T
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                                                      AGCAGTGAGGTGCTGGATGAGCTGTACCGCGCCACCAGGGGAGTTCACGCGCAGCCGCAAG
                                                                              AGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAG
                                                                                                                                       AAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGATGACACC
                                                                                                                                                                              CTGTGTCCCCCGCAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAG
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7. Tang YT, Bandmr
7. Lee S, y.
Sapperr
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autoimmune/inflammatory disorders.
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The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID No:1 to 4622); (b) the full-length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence
                                                                                                                                                                                                                                         New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cances
                                                                                                                                                                                                          Claim 1; SEQ ID NO 2473; 5504pp; English.
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) WU T D.
) ZHOU Y.
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; cell proliferative disorder; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAT) cDNA sequence #2473
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                                             CC comprising the above polypeptide fused to a heterologous polypeptide; (6) CC an isolated antibody that binds to the above polypeptide; (7) a process CC for producing the antibody; (8) an isolated oligopeptide; (7) a process CC the above polypeptide; (9) a tumour associated antigenic target (TAT) CC binding organic molecule that binds to the above polypeptide; (10) a CC composition of matter comprising the above (chimeric) polypeptide; (10) a CC composition of matter comprising the above polypeptide; (10) a CC composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of the composition of matter contained within the container; (12) methods of cinhibiting the growth of a cell that expresses the above protein, where CC therefore, the above protein in a part dependent upon a growth of the coll is at least in part dependent upon a growth of the above protein; (13) a method of determining the protein of a sample suspected of containing the protein of a sample suspected of containing the protein of a sample suspected of containing the protein of discribed above; (15) methods of diagnosing the presence of a protein; and (17) a method of reacting or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or corganic molecule to a cell that expresses the protein described above. CC The TAT sequences have cytostatic activities, and can be used in gene ct therapy. The composition and methods are useful for diagnosing, cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer. The present sequence represents a cell proliferative disorder or cancer.
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Query Match Best Local Sequence h 34.0%; Similarity 59.3%; 47; Conservative 2186 BP; 478 A; 624 C; 673 G; Score 204.2; DB 12; pred. No. 1.3e-49; 0; Mismatches 238; 411 T; 0 U; 0 Length Other; 2186

Matches

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ATCTGCGAGGCCTGGGCCGGATGCTGGACGAGGGCAGCCTCTGA 676
                               CTATGTGATGGTATCAACAAATGTTGGATGAAGAGAACATATGA
                                                                   TGCGACTTCCTGGCTGCGCTCTACGGCCCCGCCGAGCCCTACCGCTCCCACCTGCGCAGG
                                                                                                 TGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAA
                                                                                                                                        CCCCACCTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGAC
                                                                                                                                                                            CGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGAT
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RESULT 24
ADQ86751
IID ADQ86
XX ADQ86
X
                      CC sequences (see SEQ ID NO:1 to 4622); (a) the full-length coding region of CC (a); (c) the complement of (a) cor (b) d) a sequence that has 80% CC (c). Also described: (1) an expression vector comprising the above CC (c). Also described: (1) an expression vector comprising the above CC (c). Also described: (1) an expression vector comprising the above cC (c) a process for producing a polypeptide; (4) an isolated polypeptide coding region of the above encoded by any of the above comprising the above polypeptide coding region of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-cC length coding region of the above nucleotide sequence; or (c) a sequence comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (6) cr producing the antibody; (8) an isolated onligentic target (TAT) composition of matter comprising the above polypeptide; (10) a ccomposition of matter comprising the above polypeptide; (11) a ccomposition of matter contained within the container; (12) methods of the growth of a cell that expresses the above protein, where contained protein in a sample suspected of containing the protein contained above; (15) methods of diagnosing the presence of a protein in a sample suspected of containing the protein contained above; (15) methods of diagnosing the presence of a tumour in a containing and (17) a method of binding an antibody, oligopeptide or contained within containing the protein contained above. CC protein, and (17) a method of binding an antibody, oligopeptide or contained within the containing the protein contained above. CC protein, and (17) a method of binding an antibody, oligopeptide or containing the protein as contained and method of activity of the above contained and method of determining the protein contained and method of binding an antibody, oligopeptide or containing the protein as contained and cont
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   preventing or
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) WU T D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention describes an isolated tumour-associated nucleic acid comprising: (a) any of 4622 nucleoti
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   The composition is also
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RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADQ84271 standard;
                                                                                                                                                                                                                                                                       human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
                                                                                                                                                                                                                                                                                                                                                      Human tumour-associated antigenic target (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADQ84271;
                                                  15-OCT-2003; 2003WO-US029126
                                                                                                              22-JUL-2004
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                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA; 2186
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                          TAT;
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                                                                                                                                                                                                                                                                                                                                                      cDNA sequence
                                                                                                                                                                                                                                                                                                cytostatic; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an isolated tumour-associated antigenic caraget (TAT) nucleic acid comprising: (a) any of 4622 nuclectide caraget (TAT) nucleic acid comprising: (a) any of 4622 nuclectide caraget (TAT) nucleic acid; (a) or (b); (d) a sequence that has 80% sequences (see SEQ IN NO:1 to 4622); (b) the full-length coding region of caragety (c) the complement of (a) or (b); (d) a sequence that hybridises to (a)-c(c) also described; (l) an expression vector comprising the above mucleic acid; (2) a host cell comprising the above expression vector; (3) cc a process for producing a polypeptide; (4) an isolated polypeptide (c) a process for producing a polypeptide; (4) an isolated polypeptide; (6) cc a process for producing a polypeptide; (4) an isolated polypeptide; (6) cc comprising the above polypeptide; (6) a time composition of the above polypeptide; (6) cc comprising the above polypeptide; (6) cc comprising the above polypeptide; (6) cc an isolated antibody that binds to the above polypeptide; (1) a process cf for producing the antibody; (8) an isolated oligopeptide; (10) a process cf for producing the antibody; (8) an isolated altipenic target (TAT) composition of matter comprising the above (chimeric) polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide; (10) a matibody, oligopeptide or TAT binding organic molecule, in combination where composition of matter comprising the above polypeptide; (12) methods of the cappentic all that expresses the above protein, where ct potentiating the growth of a cell that expresses the above protein, where ct potentiating the proventing a container; (12) methods of containing the protein in a sample suspected of containing the protein containing the protein in a sample suspected of containing the protein containing the protein in a sample suspected of containing the protein in a method of determining the protein containing the protein and containing the protein and containing the protein of a method of containing the protein descr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-534300/51
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WU T D.
AAGAAGGAGGAGAGAAGATCAACAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATT
                                                                                                                                                                   GCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAAATCCATCGCCACCACCTTAATAGAC
                                                                                                                                                                                                                                                 CCGTCGCCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTTGGCCGTTCAG
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                                                                                                   GACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAC
                                                                                                                                        GCGCAGAAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGAT
                                                                                                                                                                                                                    CGGACTCTGCTTCGAGAGTAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAG
                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                  34.0%;
59.3%;
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Pred. No. 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                     the present invention.
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.es 238; Indels
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ABS78742 standard; DNA; 619

В₽

16-DEC-2002 ABS78742;

human NOVX17b (first entry)

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ATCTGCGAGGGCCTGGGCCGGATGCTGGACGAGGGCAGCCTCTGA
                                   CTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA 601
                                                                                                               TGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAA 556
                                                                                                                                                     CCCCACCTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGAC
                                                                                                                                                                                        CGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGAT 496
                                                                                                                                                                                                                                                                                                          CGGGCGCGCTGCCTGGCCATGACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGAC
                                                                                                                                                                                                                              CGGCGCGTGCTGGCCGGGCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGT 511
                                                                                                                                                                                                                                                                                                                                                                                   CTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAG 316
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Human; NOVX; human disease; NOVX-associated disorder; cancer; addiction; Hodgkin disease; Von Hippel-Lindau syndrome; Alzheimer's disease; stroke; tuberous sclerosis; hypercalcaemia; Parkinson's disease; depression; Huntington's disease; cerebral palsy; epilepsy; Lesch-Nyhan syndrome; multiple sclerosis; ataxia-telangiectasia; leukodystrophy; anxiety; pain; obesity; Crohn's disease; osteoporosis; inflammatory bowel disease; infertility; inflammatory bowel disease; atherosclerosis; hypertension; scleroderma; haemophilia; diabetes; pancreatitis; autoimmune disease; asthma; arthritis; immunodeficiency; HIV; viral infection; neurogenesis; bacterial infection; parastic infection; graft-versus-host disease; bacterial infection; cell proliferation; haematopoiesis; wound healing; angiogenesis; gene; ds.

08 MAR-2001; 09-MAR-2001; 12-MAR-2001; 13-MAR-2001; 13-MAR-2001; 13-MAR-2001; 20-MAR-2001; 20-MAR-2001; 20-MAR-2001; 21-MAR-2001; 21-MAR-2001; 23-MAR-2001; 23-MAR-2001; 27-MAR-2001; 2001US-0276000P. 2001US-0277239P. 2001US-027732P. 2001US-0277338P. 2001US-0277791P. 2001US-02777833P. ; 2001US-0274281P. ; 2001US-0274849P. ; 2001US-0275235P. ; 2001US-0275579P. ; 2001US-0275601P. 2001US-0278152P. 2001US-0278894P. 2001US-0279036P. 2001US-0279344P. 2002WO-US007283

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02-APR-2001; 2001US-0280802P.
02-MAY-2001; 2001US-0288148P.
31-MAY-2001; 2001US-0294821P.
31-CCT-2001; 2001US-03333075P.
04-DEC-2001; 2001US-0333375P.
04-DEC-2001; 2001US-0394466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HIV, viral, bacterial or parasitic infections, or graft-versue-host disease. The nucleic acids and polypeptides may also be used as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, cell differentiation, cell proliferation, haemopoiesis, wound healing and angiogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosme manning times.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiatelangiectasia, leukodystrophies, addiction, anxiety, depression, pain, telangiectasia, leukodystrophies, addiction, anxiety, depression, pain, telangiectasia, belake, osteoporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, infertility, inflammatory bowel disease, sterosclerosis, hypertension, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease, scleroderma, haemophilia, diabetes, pancreatitis, autoimmune disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a new polypeptide (NOVX). The NOVX polypeptide, nucleic acid and antibody are useful in the manufacture of medicament for treating a syndrome associated with a human disease, preferrably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or polypeptides and antibodies are useful for treating, preventing or diseases such as cancers, Hodgkin disease. Von Hippel-Lindau disease, and antibodies are useful for treating preventing or polypeptides and antibodies are useful for treating.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, sclerosis, atherosclerosis, cancer, infections, osteoporosis or
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                      proteins. The polynucleotides can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal and disorders such as viral infections, bacterial infections, fungal
                                                                                                                                                                                                                                                                                                                                         Five hundred and ninety two polynucleotides derived from human tissue sources which encode secreted proteins, use: immune deficiencies and disorders such as autoimmune dis
                                                                                                                                                                                   The invention relates to 592 polynucleotides which have k a variety of human tissue sources and which encode novel
                                                                                                                                                                                                                                                                                  Claim
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Best Local (
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                              Human; secreted protein; atherosclerosis; Alzheimer's disease; LP237; diabetic retinopathy; severe combined immunodeficiency; pancreatitis; rheumatoid arthritis; colorectal adenoma; haemolytic anaemia; cancer; reperfusion injury; arteriosclerosis; wound healing; transgenic animal;
                                                                                                                                                                                                                                                   AAD38699
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                                                                                                                                    Human
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                therapy;
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                                                                                                                              secreted protein
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                                                                                                                                encoding cDNA.
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                  psoriasis;
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                                                                                                                                                                                                                                                                                                                                        The invention relates to human secreted polypeptides designated LP095, LP219, LP217, LP220, LP221, LP222, LP229, LP237 or LP338 and nucleic acid molecules encoding such polypeptides. Novel secreted proteins of the invention are used for treating diseases such as atherosclerosis, atheroscierosis, retinopathy, psoriasis, pancreatitis, attributed immunodeficiency, ischaemia, carcinomas, haemolytic anaemia, reperitusion injury, neoplasms and cancer especially liver cancer. They are also used for wound healing. Polymucleotides of the invention can be used to generate transgenic animals or knock out animals, which in turn, are useful in the development and screening of therapeutically useful reagents for use in the treatment of diseases associated with LP polypeptide associated activity. They are also used in gene therapy. The present sequence is human LP237 secreted protein encoding cDNA
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Matches 336
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                                                                                                                                                                                                                                                                                                                                        Sequence 1165 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel proteins and polynucleotides of secreted proteins useful for treating various diseases e.g. rheumatoid arthritis, cancer, psori
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                                                                        AGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATA
                                                                                                     AGGTGCTAGATGAGCTCTACCGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCC
                                                                                                                       AGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAAACAAGAAGGAGGCAG
                                                                                                                                                             TACTGAGTAAGATGGCGGGTCGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTG
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                                                                                                                                                                                                                   cTccaggacccaTggagtccTTcagcTcaaagagcCTggcaCTgcaagcagaagaagaagc
                                                                                                                                                                                                                                                CTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retinopathy, arteriosclerosis, ischemia or reperfusion injury
                                             AGCGCGTGATCAAGGACCTGATCAAAGTGGCCATCAAGGTGGCTGTGCTGCACCGCAATG
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                                                                                                                                                                                                                                                                                                                                        305 A; 319 C; 312 G;
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3.7e-43;
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The invention relates to an isolated polynucleotide (I) comprising a nucleotide sequence selected from any of 948 sequences (ABZ11119-ABZ12066) or their mature protein coding portion, active domain coding protein or complementary sequences. The polynucleotides are useful for identifying expressed genes or for physical mapping of human genome. The
                                                                                                                                                                                                                                                    New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-SEP-2002
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Ma Y, Yamazaki V, Chen
, Wang D, Drmanac RT;
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         TCAACAAATGTTGGATGAAGAGAACATATGA
                                           CGGCCCTCTATGGGCCT-----GACTTCACTCAGCACCTTGGCAAGATCTGTGACGGAC
                                                                             CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA
                                                                                                                 CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCAGGTCTGCTCA
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Pred. No. 3.7e-43;
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Matches 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/c treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated arginine-rich protein-like polynucleotides and useful for diagnosing and/or treating conditions associated activity of the arginine-rich polypeptides, such as cancer activity.
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05-MAR-2002; 2002WO-US005095
20-AUG-2002; 2002US-00225251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human arginine-rich protein cDNA.
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                                                                                                                                                                        GCTCCTTTGGCCCCAGTGAGCTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGG
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                          CCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGG
                                                                                 CCAGGCTGTTAAATGAATGCAGAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTG
                                                                                                                 GTGCCATGACGGCACTTAGCTTTGGTGAGGTAGACTTCACCTTCGAGGCTGCTGTTCTGG
                                                                                                                                             TTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTAT
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CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCAGGTCTGCTCA
                                                       CTGGCCTGCTGACCGAGTGCCGGGATGTGCTACAGTTGGTGGAACACCACCTCACGC
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Pred. No. 3.7e-43;
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CC Sequences AAF59590-AAF59643 represent cDNAs encoding 54 human cell cycle CC and proliferation proteins (CCYPR), AAB60453-AAB60506. CCYPR and agonists CC of CCYPR are used to treat diseases or conditions associated with cCC decreased expression of functional CCYPR, while CCYPR antagonists are CC used to treat diseases or conditions associated with overexpression of functional CCYPR. Monoclonal or polyclonal antibodies to CCYPR may be used in enzyme-linked immunosorbent assays (ELISA) or radioimmunosays to CC detect CCYPR. CCYPR itself may be used to detect compounds e.g., CC antibodies, oligonuclectides and proteins (receptors) that specifically bind to CCYPR, and in drug screening methods to identify compounds that compounds that modulate the activity of CCYPR. CCYPR nucleotides can be used to generate thrangenic animal models of human disease, and can be used in gene compounds that the compounds of CCYPR. CCYPR nucleotides can be used to generate thrangenic animal models of human disease, and can be used in gene compounds that compounds that compounds that the protein compounds that the associated with CCYPR. Diseases which can be disorder animal models of the proteins include anaemia, epilepsy, arterioscis, agonists or antagonists compounds cell concers. Specific examples of these construed using disorders include anaemia, epilepsy, arteriosclerosis, asthma, cancer, confections caused by bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                    Human cell cycle and proliferation proteins and polynucleotides are used to treat, diagnose and prevent immune, developmental and cell signaling disorders and cell proliferative disorders including cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell cycle and proliferation protein; CCYPR; human; agonist; antag gene therapy; detection; gene therapy; transgenic animal disease m immune disorder; developmental disorder; cell signalling disorder; cell proliferative disorder; cancer; tumour; anaemia; epilepsy; arteriosclerosis; asthma; allergy; diabetes mellitus; menstrual cycle disorder; bacterial infection; ss.
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08-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                  Human; probe; ss; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
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                                                                                                                                                       03-APR-2002; 2002US-00029386
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CC sequences (optionally with conservative amino acid substitutions), an CC isolated antibody that binds specifically to a peptide cited above, CC methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing CC acustomer desiring to measure gene expression, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe coited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying ctissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. CC in addition, the probes are used in identifying and characterising cc alternative splicing events, in detecting and characterising gross calterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, cor in expressing the ORF-encoded peptide. The present sequence is a human csingle exon morbe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained contained across the cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid probe for measuring human gene continues of the 27,400 fully defined nucleotide content of the specification, or their complements or fragments, and concoling at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that the specification of the specification of the probe is a single exon probe that the specification of the probe is a single exon probe that the specification of the probe is a single exon probe that the specification of the probes is a single exon probe that the specification of the probes is a single exon probe that the specific acid probes for measuring human concoling the single exon nucleic acid probes for measuring human concoling at least the plurality of single exon nucleic acid probes is separately and addressably isolatable or amplifiable from the plurality, a single exon microarray for measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising the single exon contiguous amino acids of any of the above mentioned amino acid of contiguous amino acids of any of the above mentioned amino acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human genome-derived single exon nucleic acid probes useful gene expression analysis, for identifying or characterizing altesplicing events, for assessing genomic alterations or as tools is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 15; SEQ ID NO 9211; 80pp; English
                                                               seqdata.uspto.gov/sequence.html?DocID=20030194704
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AAC10352
ID AAC10
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AC AAC10
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                    AAC10352 standard; cDNA; 340
                    ВP
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492 61

CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTAC

551 60 491

120

CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCCACTTAC

AAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATATGA 601

Matches 169; Query Match

Conservative

0

432 TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTT

TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTGATCATTTTT

Local Similarity

28.0%;

Score 168.4; Pred. No. 2.6 Mismatches

.6e-39; DB 12;

Indels Length Other;

<u>.</u>

Gaps

Sequence 500

BP; 164 A; 71 C; 107 G; 158 T; 0 U; 0

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RESULT 34
ABL07183
ID ABL07
XX
AC ABL07
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DT 26-MI
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                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                     mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic NAS. 5' ESTs are also used in
Drosophila melanogaster expressed polynucleotide SEQ ID NO 16031
                                                                                                                                                                                                                                                                                                                 Sequence 340 BP;
                                                                                                                                                                                                                                                                                                                                       expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wew nucreate acta that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP1033401-A2
                                                                     ABL07183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 14427; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500381/45
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                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                 nostic, forensic, gene therapy and chromosome mapping are used to obtain upstream regulatory sequences and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy;
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                                                                                                                                                                       TGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGC
                                                                                                                                                                                                                     ATGTCTTTAATTCCAAAAAACCTGGCCGKTCAGGCACAAAARAAGATCTTGGGTAAAATGG
                                                                     standard;
                                                                                                                                                                                        TGTCCAAATCCATCGCCACCACCATTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGC
                                                                                                                                                                                                                                             ATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGG
                                                                                                                           TCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is one of a large number of 5' ESTs derived fing secreted proteins. No ORF has yet been conclusively within the present sequence. The 5' ESTs were prepared
                                                                                                                                                                                                                                                                  26.5%;
ilarity 98.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic, gene therapy and chromosome mapping procedures.
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                        (first entry)
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                                                                                                                                                                                                                                                                                                                 A; 79 C;
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                                                                                                                                                                                                                                                                 Score 159.2; DB 3
Pred. No. 1.2e-36;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                 85 G;
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Matches 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 829 BP; 229 A; 208 C; 210 G; 182 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 16031; 21pp + Sequence Listing; English
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                                                                       383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCACGCATGGCCACAAAAAACATCGCCAAGACCTTCATCGATGGCACGACGGCGTCGCTG
TCAATAGCCGAATCGCAAGTGGCGCTGAAGTCGATTTGTGCAGCCGCATCTCACAGAAAAG
                                                                                                                                              ATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTTGACCGGAATGTGTTATCCAGG
                                                                                                                                                                                                                       TTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCT
                                                                                                                                                                                                                                                                                       CTGATCAAGAACATCATCAAGATTGTGATCAAGATCGGTGTGCTCCACCGGAACAATCAG
                                             CTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAG
                                                                                             CTGTCCATCATATCATTCTACGAAGTGGACTTCACGTTCGACCTGCCGTACCTGCAAAAG
                                                                                                                                                                                           TTCAGCGACGAGGAGCTGCAGAAGGCGGAGCTCTTTAAGAGAAAGTTTCAAAACACGCAG
                                                                                                                                                                                                                                                                                                                                                                                       CTGGACAACCTCTACAGGCTCTGCAAGATGCACACGGGGAACAAGGCCAAGGCGGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTG
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Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polynucleotide comprising any one of C3 88043 cDNA sequences, appearing as ACHI-2789-ACH59831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is one of the 38043 isolated CDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                             Query Match
Best Local
                                                                                                                  Matches
                                                                                                                                                                                                                               Sequence 422 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome
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                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20030073623
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) DICKSON M C.
) JONES L W.
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CTCCAGGACCCATGGAGTCCTTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAGAAGAAGC
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                                                    CTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGA
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                                          The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. ESTs are derived from mRNAs with intact 5' ends and can therefore be us to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                     diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                       Dumas Milne Edwards
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                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 14434; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
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                               expression and secretion vectors
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                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano
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AAK56622

ID O6-NC

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Best Local Similarity
Matches 138; Conserv
    26-JUL-2000;
26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
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  2000US-018464P.
2000US-019874P.
2000US-019974P.
2000US-020511P.
2000US-021513P.
2000US-021513F.
2000US-02151486P.
2000US-021647P.
2000US-021648P.
2000US-021648P.
2000US-0218290P.
2000US-0218290P.
2000US-02284518P.
2000US-0228518P.
2000US-0225214P.
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98.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 126.4; DB 3
Pred. No. 5.4e-27;
0; Mismatches 1
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| 2000US-0228924P.
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| 2000US-022934P.
| 2000US-023943P.
| 2000US-023943P.
| 2000US-0231243P.
| 2000US-0231413P.
| 2000US-0231413P.
| 2000US-0231414P.
| 2000US-0232981P.
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| 2000US-0232981P.
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Matches 194
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                                                                                                                                                                                                                             expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic delis. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                     AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis ar treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic useful for preventing, diagnosing and/or treating
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17-NOV-2000;
                                                                                                                                                                                     Sequence 441 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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                                                                                                                         194;
                              99
                                                           78
                                                                                                                                       Similarity
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                             AAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1682; 3071pp + Sequence Listing; English.
AGATGGCGGGTCGCTCTGTGGCTCATCTCTTCATAGATGAGACAAGCAGTGAGGTGCTAG
                                                                             CCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTA
                                                                                                                                                                                                                  sequences
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2000US-02492119
2000US-0249214P
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2000US-0249218P
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2000US-0251869P.
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2000US-0251988P.
2000US-0256719P.
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2000US-0251856P.
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                                                                                                                                                                                      99
                                                                                                                                                                                   A; 119 C; 127 G; 89 T; 0 U; 7 Other;
                                                                                                                                                                                                                   used in the exemplification of the
                                                                                                                                      19.7%;
59.3%;
                                                                                                                       ω
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                                                                                                                                       Score 118.4; DB 4
Pred. No. 1.7e-24;
                                                                                                                         Mismatches 130;
                                                           CTGCAAGCAGAGAAGAAGCTACTGAGTA
                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen polypeptides, cancers and metastasis.
                                                                                                                         Indels
                                                                                                                                                    Length
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the

Gaps

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9 TCCCGGCGCCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAAACCTGG 68

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RESULT 38
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Query Match
Best Local Sim
Matches 191;
                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventior useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIG176-ABIG3051), expressed DNA sequences (ABIG1840-ABIG175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL07182 standard; cDNA; 4406
                                                          Sequence 4406 BP;
                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 16028; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                              New isolated nucleic a genes from Drosophila
                                                                                                                                                                                                                                                                                                                                                                                    Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                  interactions
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               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCCAGTGAGCTGGCCCTGGCTAMCCGCTTTCGCCAGAARCTGCGGCAAGGTGCCATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTATAGGAATAATCAGTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAGCTCTACCGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCCAGCGCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     melanogaster expressed polynucleotide SEQ ID NO 16028
                                                                                                                                                                                                                                                                                                                                                                                    Adams M,
 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene;
                                                        1178 A; 1021 C; 1027 G; 1180 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                              acid
a and
             19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                     PWD,
                                                                                                                                                                                                                                                                                            detection reagent for detecting 1000 for elucidating cell signaling and ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biology; cell signalling; insecticide;
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               Score 116; DB 4;
Pred. No. 2.8e-23;
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                                                                                                                                                                                                                                                                                                                                                                                     Myers EW
Mismatches
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 125;
                          Length 4406
 Indels
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 Gaps
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RESULT 39
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ID AN1924
XX AN1924
XX AN1924
XX Human
DT 06-NOV
DE Human
XX Human;
KW Vaccin
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAQ00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, tissue growth factor activity, immunomodulatory activity and activity/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                   and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nervous system disorders;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide SEQ ID NO 12495
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                                                                                                                                                                                                                                                                                                                 nucleic acids and polypeptides, ting e.g. leukemia, inflammation
                                                                                                                                                                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGGGAACAAGGCCAAGGCGGAGAAGCTGATCAAGAACATCATCAAGATTGTGATCAAGA 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCATCGATGGCACGACGGCGTCGCTGCTGGACAACCTCTACAGGCTCTGCAAGATGCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTGCGGGCGCAGAAGAAGATCCTCTCACGCATGGCCACAAAAAAACATCGCCAAGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                   NO 12495; 1399pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell differentiation;
                                                                                                                                                                                                                                                                                                                 , useful for and immune
                                                                                                                                                                                                                                                                                                                   preventing disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy;
                                                                                                                                                                                                                                                                                                                                  diagnosing
                                                                                                                                                                                         induce
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                                                                                                                                                  OF,
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Matches
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                                                                                                                                                       Ota T,
                                                                                                                                                                                                               29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                       28-JUL-2000;
                                                                                                                                                                                                                                                                        EP1074617-A2
                                                                                                                                                                                                                                                                                                      Human;
                                                                                                                                                                                                                                                                                                                       Human
                                                                                                                              WPI; 2001-318749/34.
                                                                                                                                               Ishii
                                                                                                                                                                                              02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                       AAH04721;
                                                                                                                                                                                                                                                                                                                                                                       AAH04721
                                                                                                                                                                        (HELI-)
                                                                                                                                                                                                                                                                                                                                       26-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                       40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                       CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
                                                                                                                                              Isogai T,
3, Sugiyama
                                                                                                                                                                                                                                                                                                      primer;
                                                                                                                                                                       HELIX RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           GAGGCAGAGAAGATCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                GAGGCCCAGAAGATGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAGCTCCTGAGTAAGATGGCGTCCAAGGCAGTGGTGGCCGTGCTGGTGGATGACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGTGTCCCCCGCAGGCCATGGACACCTTCAGCACCAAGAGCCTGGCTCTGCAGGCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGACTCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                               AGCAGTGAGGTGCTGGATGAGCTGTACCGCGCCACCAGGGAGTTCACGCGCAGCCGCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400
                                                                                                                                                                                                                                                                                                                      clone (5'-primer)
                                                                                                                                                                                      ; 99JP-00248036.
; 99JP-00300253.
; 2000JP-00118776.
; 2000JP-00183767.
; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                       2000EP-00116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B₽;
                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                     detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                        INST
                                                                                                                                              Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                      CDNA;
                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; 122 C; 114 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.6%;
                                                                                                                                                                                                                                                                                                                                                                      714
                                                                                                                                                                                                                                                                                                                      SEQ
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                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99.8; DB 4;
Pred. No. 5.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                             Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                       IJ
                                                                                                                                                                                                                                                                                                                       NO:1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 T; 0 U;
                                                                                                                                              Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                               H
                                                                                                                                                       Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                              202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
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nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides, or (b) a combin of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end

combination

The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary to the

Primer sets for synthesizing polynucleotides, length cDNAs defined in the specification, and diagnosis of the abnormality of the proteins of the abnormality of the proteins of the proteins of the abnormality of the proteins of

and

, particularly the 5602 full-nd for the detection and/or encoded by the full-length

Claim

1; SEQ ID

NO 1556; 2537pp + Sequence Listing; English.

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Matches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods AHH33166 to AHH3628 and AHH3331 to AHH89742 represent human cDNA sequences; AHB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
  Ota T, :
Ishii S,
                                                                                                                      29-JUL-1999; 99JP-00248036.
27-AUG-1999; 99JP-0030253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human cDNA sequence SEQ ID NO:18986.
                                                                                                                                                                                                                                                                                                                                                                EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAH18715 standard; cDNA; 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 714 BP; 113 A; 246 C; 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JUN-2001
                                                                                                                                                                                                                                                                     28-JUL-2000; 2000EP-00116126
                                                                         (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer;
                           Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAATGAATGCAGAGAGAGGCTGCCCCCAAATCATTCAGCGCCACCTCACTGCCAAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCTGGACGAGGGCAGCCTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGGCCCCGAGCCCTACCGCTCCCACCTGCGCAGGATCTGCGAGGGCCTGGGCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis;
                           Nishikawa T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
    Wakamatsu
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263
Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.4;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T; 0 U; 4 Other;
  Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 714;
                           Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13631 to AAH18742 represent human aclid sequences; ABB2446 to AAB95893 represent human acid sequences; and AAH13632 represent oligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length cDNAs defined in the specification. Where a primer set comprises:
(a) an oligo-dl primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                               present invention
     459
                                                    61
                                                                                                                                                                               CCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGCTGT
                                                                                                                                                                                                                                                                                                                                             1602 BP; 334 A; 458 C; 491 G; 319 T; 0 U; 0 Other;
     ATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCTTGT
                                                       TGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTCCC
                                                                                                 TAPATGAATGCAGAGAGAGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCAC
                                                                                                                                                   CGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGCGCGTGCTGGCCGCCGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO 18986; 2537pp + Sequence Listing;
                                                                                                                                                                                                                                                                       14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        describes primer
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                       Score 85.4; DB 4;
Pred. No. 2e-14;
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sets
                                                                                                                                                                                                                                                111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for synthesising 5602 full-
                                                                                                                                                                                                                                                                                             Length 1602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                Gaps
       518
                                                       120
                                                                                                      458
                                                                                                                                                   60
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X 5 X F X B X B X S X X X
                           Human;
                  splice variant;
                                                                                                            ABN50404 standard;
                                                                     15-JUL-2002
                           mouse; rat; splice transcript; detection; RNA transcript;
                                                                    (first entry)
                                               transcript
                 transcriptome;
                                                                                                            DNA; 60
                                               detection oligonucleotide
                 oligonucleotide
                                               SEQ
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ID NO:23152

δ 밁 S 밁

TGCTGGACGAGGGCAGCCTCTGA TGTTGGATGAAGAGAACATATGA 181

121

ACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGACTGCGACTTCCTGGCTGCGCTCT

ACGGCCCGCCGAGCCCTACCGCTCCCACCTGCGCAGGATCTGCGAGGGCCTGGGCCGGA ATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAA

240 578

180

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RESULT 43
ACF25360
ID ACF25
XX ACF25
XX ACF25
XX ACF25
XX ACF25
XX BRAT TACK
XX BPINA
XX BPINA
XX ARALL
XX RALL
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                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                 rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not for part of the printed specification, but was obtained in electronic for directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of
                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN39589 represent oligonucleotide sequences from
                                                                                                                                                                                                                                                                                                                                                                                                                                                           biological or pathological state, and so allowing the detection of tissue - and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
                                                                                                                                                              ACF25360 standard; DNA; 7095 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-2000; 2000US-0221607P
02-MAY-2001; 2001US-0287724P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-FEB-2002
              Rattus norvegicus
                                          analgesic;
                                                     spinal
                                                                              Rat microtubule associated protein IB gene
                                                                                                          22-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               messenger RNAs transcribed from a given transcription unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 23152; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specific
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUL-2001; 2001WO-IB001903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200210449-A2
                                                                                                                                                                                                                                              199 GAAGGAGGAGGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCT
                                                                                                                                                                                                                                                                                   60;
                                                   cord; neuropathic pain;
                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                               GAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCT
                                        gene
                                                                                                                                                                                                                                                                                                                                        BP; 22
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                                                                                                                                                                                                                                                                                    Conservative
                                                                                                         (first entry)
                                       therapy;
                                                                                                                                                                                                                                                                                                                                        A; 14 C; 14 G; 10 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                             10.0%;
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                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                       gene;
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                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                 Score 60;
Pred. No.
                                                     central sensitisation pain; pain;
                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                             but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mintz
                                                                                                                                                                                                                                                                                   1.3e-07;
hes 0;
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RESULT 44
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         downregulated in the spinal cord of a mammal in response to mechanically distinct first and second models of neuropathic or central sensitisation pain, useful in the screening of compounds for diagnosing or treating pain. A protein encoded by a gene of the invention has analgesic activity. A polynucleotide of the invention may have a use in gene therapy. The gene sequence is useful for preparing a composition for diagnosing or treating pain. The present sequence represents a gene of the invention.
alternative splicing event; genomic alteration
                                                                                                    29-JUL-2004
                                                                                                                                             ACH78513;
                                                                                                                                                                                      ACH78513 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7095 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated gene sequence that is downregulated in the spinal cord of a mammal in response to mec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 125-127; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of an isolated gene sequence diagnosing or treating pain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brooksbank
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07-FEB-2002; 2002GB-00002883
                   Human; probe; ss;
                                                          Human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                  293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 TCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129;
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                                                                                                                                                                                                                                                                                           GAACCCAAAAAGGAGATTAAGAAGA 1909
                                                                                                                                                                                                                                                                                                                                  GCATTGATGGAGAAATTTAAGAAGA
                                                                                                                                                                                                                                                                                                                                                                             AAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATCAAAAAGGAAGAAAAAGGAGCTGAAGAAAGAGGTGAAGAAGGAAACGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAACCCGAAGAAAAGAAGAGGAAGCCCCAAGAAGGAAGTGGCTAAAAAGGAAGACAAA
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                                                        derived single exon probe #11708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002EP-00255229
                                                                                                 (first entry)
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                   gene expression; single exon probe; microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2124 A; 1856 C; 1799 G; 1316 T; 0 U; 0 Other;
                                                                                                                                                                                      DNA; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%;
48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1704
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US2003194704-A1

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                                                                                                                                                                                                                                                                                     CC gene expression (comprising a plurality of single exon nucleic acid gene expression (comprising a plurality of single exon nucleic acid comprobes cited above, where each of the plurality of probes is separately cand addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of commicroarray for measuring human gene expression, a method of comprising human gene expression, a method of comprobe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid substitutions), an constiguous amino acid substitutions and comprobe of selling and/or licensing single exon probes or microarrays to contiguous antibody that binds specifically to a peptide cited above, contains and comprobes or microarrays to a customer desiring to measure gene expression, a method of providing thuman gene expression data by subscription, and a computer-readable contains a database having a plurality of records cexpression analysis. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. Constructing genome-derived single exon microarrays. Constructions in the genomic locus that includes that exon, in assessing confidence in the probes are used in identifying and characterising gross alterations in the genomic locus that includes that exon, in assessing the original exon probe of the invention. Note: The sequence is a human confidence of the invention, but was obtained confidence of the invention of the printed specification, but was obtained confidence in electronic format directly from USPO at
                                                                                                                                                                                      Query Match
Best Local S
Matches 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PENN/) PENN S (RANK/) RANK D I (HANZ/) HANZEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or ragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                              Sequence 543 BP; 137 A; 128 C; 119 G; 159 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 15; SEQ ID NO 11708; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-2002; 2002US-00029386
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                                                                                                                                                                                                                                                                                                                            seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-119264/12
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    61
                                                                                                                                                                                                         Similarity
                                           АТААТССТТТТGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAA
                                                                                                                                   ATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGT
ATAGTCTGGATGGAGACTGTAGGCCCAACCTCAAGAGGATTTGTGAAGGAATCAATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR,
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                                                                                                                                                                                      Conservative
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พ.
                                                                                                                                                                                                         58.0%;
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                                                                                                                                                                                                                                  7.8%;
                                                                                                                                                                                    ,
,
                                                                                                                                                                                                         Score 47;
Pred. No.
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                         0
                                                                                                                                                                                                                               DB 12;
                                                                                                                                                                                                            .0029;
                                                                                                                                                                                      60;
                                                                                                                                                                                                                               Length 543;
                                                                                                                                                                                      Indels
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                                                                                                                                                                                    Gaps
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RESULT 45
AB076615/c
ID 76615/c
XX AB076
XX AB07
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                                                              candida spp. sequences that are differentially expressed in a pathway eventually leading to programmed cell death or identifying inhibitors or inhibitor sequences of Bax-induced cell death. The products of the cinvention have cytostatic, fungicide; immunosuppressive, virucide and vasotropic activity and can be used in vaccines or for gene therapy. The isolated nucleic acids, polypeptides, pharmaceutical compositions, antisense molecules and antibodies are useful as medicaments or in preparing a medicament for treating, preventing and/or alleviating preparing a medicament for treating, preventing and/or alleviating compositions, or in associated with yeast or fungi or proliferative disorders, such as cancer, or for preventing apoptosis in certain diseases. The compounds or polypeptides, or the genetically modified organism are useful for preparing a medicament for modifying the endogenic flora of humans and other mammals. The vaccine is useful for immunising against yeast or fungal infections. Apoptosis-related diseases include autoimmune disease, ischaemia, diseases related with viral infections or neurodegenerations. This sequence represents a polynucleotide associated with the Bax gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 36; Fig 2; 344pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid representing a synthetic BAX-gene, useful as medicament for treating, preventing and/or alleviating yeast or fungal infections or proliferative disorders, or for preventing apoptosis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-2000; 2000EP-00870318
04-JAN-2001; 2001EP-00870002
09-JAN-2001; 2001EP-00870003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes a novel nucleic acid representing
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Sequence 205411,
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Sequence 5, Appl,
Sequence 5, Appli
Sequence 430, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1529, Ap
Sequence 1123, Ap
Sequence 1, Appli
Sequence 1747, Ap
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Sequence 1623, Ap
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51511, Ap
51600, Ap
51388, A
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725, App
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US-09-799-451-537
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 537
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APPLICANT: Tang, Y. Tom
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CURRENT APPLICATION NUMBER: US/09/799,451
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TITLE OF INVENTION: No. 6783969e1
TITLE OF INVENTION: Polypeptides
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
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Zhou, E.
Zhou, E.
Goodrich, K,
Asundi, Vinod
Ren, Felyan
Tay, Jie
Tay, Jie
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
CCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTG 449
                               GTGCCATGACGGCACTTAGCTTTGGTGAGGTAGACTTCACCTTCGAGGCTGCTGTTCTGG
                                                             TTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTAT 389
                                                                                             GCTCCTTTGGCCCCAGTGAGCTGGCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGG
                                                                                                                                                                                        AGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATA 269
                                                                                                                                                                                                                                               AGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAG
                                                                                                                                                                                                                                                                                        TACTGAGTAAGATGGCGGGTCGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTG
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Chen, Rui-hong
Wang, Zhiwei
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Ghosh, Reena
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man, Tom
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SOPTWARE: Patent.pm
SEQ ID NO 14427
LENGTH: 340
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                                                                                                                                                                                 Matches
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Best Local Similarity
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CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
'COATION: 170
'Teature
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 139
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LOCATION: 208
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NAME/KEY: misc_feature
LOCATION: 166
OTHER INFORMATION: r=a
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TCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGA
                                                                     TGTCCAAATCCATCGCCACCATCAATAGACGACACAAGTAGTGAGGTGCTGGATGAGC 164
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                                                  TGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGC
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Pred. No. 4.7e-40;
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US-09-513-999C-14434
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Best Local Similarity
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SEQ ID NO 14434
LENGTH: 252
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TITLE OF INVENTION: Expressed Sequence Tags
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
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APPLICANT:
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PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 5
CLASSIFICATION: 435
                                 APPLICATION NUMBER:
                                                                                                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                     14, Application US/08232463
o. 5670367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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                                                                                                                                                22313-0299
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Alexandria
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                                                                                                                                                                    USA
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                                                                                                                                                                                                                                  Foley & Lardner
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RESULT 5
US-09-248-796A-4857
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                             GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
                                                                                                                                                                                                                                          Sequence 4857, Application US/09248796A Patent No. 6747137
SEQ ID NO 4857
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INFORMATION FOR SEQ ID NO:
                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         341 GTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCTGTTA 400
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US-09-489-039A-1361
; Sequence 1361, Application US/09489039A
; Patent No. 6610836
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US-09-436-699C-19
                RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 1361
LENGTH: 804
TYPE: DNA
ORGANISM: Klebsiella
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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NAME/KEY: unsure
LOCATION: (50)
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                                                                                                         A 363
                                                                                                                                         AGGAAAAACTGGAAAAAGATCCGCGCATCGCTGCCACCATGGCGAACGCCCAGAAAGGCG
                                                                                                                                                                         AGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGTGG 362
                                                                                                                                                                                                                 AGGGTCTGGAAGCCGTTAACAACGACAAACCGCTGGGTGCCGTGGCGCTGAAATCCTTCC
                                                                                                                                                                                                                                                   TCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGG 302
                                                                                                                                                                                                                                                                                       CCGCCAGCCCGAACAAAGAGCTGGCCAAAGAGTTCCTCGAAAACTACCTGATGACCGATC
                                                                                                                                                                                                                                                                                                                         AGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCA 242
                                                                                                                                                                                                                                                                                                                                                            CAACCTTTAAAAGGCAAACCATCGAAACCGTTCGTTGGCGTGCTGAGCGCGGGGATCAACG
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Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Complete Genome Sequence Patent No. 6503729

TITLE OF INVENTION: jannaschii FILE REFERENCE: PB275

CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT FILING DATE: 1997-08-22

PRIOR APPLICATION NUMBER: US 60/024,428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Microsoft Office 97
SEQ ID NO 19
LENGTH: 1719
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08916421B Patent No. 6503729
                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
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NAME/KEY: misc_feature
LOCATION: (84808).. (84808)
OTHER INFORMATION: n equals a
NAME/KEY: misc_feature
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APPLICANT: Simmons, Carl
TITLE OF INVENTION: Plant Aminoacyl-trna Synthetases
FILE REFERENCE: BBL266 US NA
CURRENT APPLICATION NUMBER: US/09/436,699C
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: 60/107,276
PRIOR APPLICATION STATE: 1998-11-05
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
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NUMBER OF SEQ ID NOS: 3
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NAME/KEY: misc_feature
LOCATION: (28222)...(28222)
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LOCATION: (84773)..(84773)
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LOCATION: (28257)..(28258)
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LOCATION: (309398)...(309398)
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LOCATION: (779455)...(779455)
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US-09-692-570-1/c
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TITLE OF INVENTION: Complete Genome Sequence
Patent No. 6797466
TITLE OF INVENTION: jannaschii
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CURRENT FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: US 60/024,428
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PRIOR APPLICATION NUMBER: US 08/916,421
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                                 NAME/KEY: misc feature
LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals
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LOCATION: (98159)..(98159)
OTHER_INFORMATION: n equals
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals
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LOCATION: (28257)...(28258)
OTHER INFORMATION: n equals
FEATURE:
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OTHER INFORMATION: n equal
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LOCATION: (84808)..(84808)
OTHER_INFORMATION: n equals
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 NAME/KEY: misc_feature
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LOCATION: (312837)...(312837)
OTHER_INFORMATION: n equals
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals
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LOCATION: (559167)...(559167)
OTHER INFORMATION: n equals
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals
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LOCATION: (312993)..(312993)
OTHER INFORMATION: n equals
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals
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LOCATION: (234814)..(234814)
OTHER_INFORMATION: n equals
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals
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LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals
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LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals
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LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals
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LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals
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LOCATION: (98343)..(98
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NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER_INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc feature
(1096846)..(1096846)
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NAME/KEY: misc_feature
1084830)..(1084830)
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals
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LOCATION: (657081)...(657081)
OTHER_INFORMATION: n equals
OTHER INFORMATION: n equals a,
           NAME/KEY: misc feature LOCATION: (1349473)...
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LOCATION: (871619)..(871619)
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals
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LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals
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LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals
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LOCATION: (682442)..(682442)
OTHER_INFORMATION: n equals
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LOCATION: (674435)...(674435)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (622708)..(622708)
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SOFTWARE: Patent.pm
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Best Local Similarity 48.1%;
Matches 104; Conservative
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CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Dumas Milne APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 235..399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 832
TYPE: DNA
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 301
                                                                                                                                        181 WWYCWWWGKARKWSTWRKSRSYASARSAKRCCYSCSWGAMSWKYMWRMWRWRGWATGAGM
                                                                                                                                                                           419 CTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTC
                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                361 GGATTATACCTTTGACCGGAATGTG--TTATCCAGGCTGTTAAATGAATGCAGAGAGATG
                                                                                                                                                                                                                                                                                                                       301 GGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGGT
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                                                                                                                                                                                                                                                                                                                                                           1 YRWYWWKYTTWYAKCWTKWKWSYWMYWKWYYMKTYWRWRRKKKKAWWKYWKTWTWWYW
 ASKKYMWKRWWWCWARMYRYSTGTRASMWWRRWYYTMMMKWWKYAWARAAWRWWAMWWAW
                                 AAACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAGAACATA
                                                                   KAWRASCYMRRKYAGKSKTSYKSMWMCWTRSWKYCYTKARWTGYYCYRKGGMWGKRGRWY
                                                                                                    TTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTT
                                                                                                                                                                                                               YRCWKKKAYYRKTTCYSSKGWTWWKRWKKAWTTWWWKKTYYWAATRYWWMMCWTKRWRAS
                                                                                                                                                                                                                                                                                    RYAMWGTYKKKAMCRTKTKKKKKKKKGYMWMWYWGWRRSYMAMWTRTWTGYAYYRSMMYWWR
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Pred. No. 0.46
65; Mismatches
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; NAME/KEY: misc feature
; LOCATION: (1)...(161900)
; OTHER INFORMATION: n = A
US-09-949-016-12685
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US-09-949-016-12685/c
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                                                                                                                                   GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
SOFTWARE: Fast
SEQ ID NO 12906
                                                                                                                                                                                                                                                                                                                                               Sequence 12906, Application US/09949016 Patent No. 6812339
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SEQ ID NO 12685
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Best Local Similarity
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                                                                                  PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                            NUMBER OF SEQ ID NOS:
                                                                   PRIOR FILING DATE:
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PRIOR FILING DATE: 2000-09-08
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RESULT 14
US-09-270-767-7337/c
; Sequence 7337, Application US/09270767
; Patent No. 6703491
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APPLICANT: ANAUT, Greta
APPLICANT: DAMME, Nicole
ITITLE OF INVENTION: No. 6706860el Toxins
FILE REFERENCE: 021565-091
CURRENT APPLICATION NUMBER: US/09/858,5258
CURRENT APPLICATION NUMBER: US 09/573,872
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 12
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US-09-858-525B-9
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Best Local Similarity
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LOCATION: (3)..(2510)
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OTHER INFORMATION: n =
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                                                                                                                                                                                                                                                                           98 AAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTG
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                                                                                                                                                                                                        GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATC 217
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Pred. No. 1;
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Pred. No. 11;
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Best Local Similarity
Thes 83; Conserv:
                                                                                            US-09-949-016-23836/c
                                                                                                                RESULT 16
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US-09-270-767-22619/c
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; ORGANISM: Drosophila melanogaster
US-09-270-767-7337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22619
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7337
                                                         Sequence 23836, Application US/09949016 Patent No. 6812339
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Best Local Similarity
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TYPE: DNA
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                                                                                                                                                              GTTGATTACTTGTAAATACGTTTTGTCAGCTTGAAACCGCA 238
                                                                                                                                                                                                TTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCA 546
                                                                                                                                                                                                                                   CCAGTAAACCCACAGATATGTGTTGTGTTTGTCATTTTTGTATTTTTTGGTTGCTTGGTTG
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Pred. No. 0.45;
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US-09-949-016-23836
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 173088
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                                                                                                                                                                                                                                         Query Match
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SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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304 GAAATTTAAGAAGAAAGTTCATCAGCTTGCTAT 336
                                                                           244 CAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGA 303
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                                                                                                                   GAACAACACCATCAAAAAGTAGGCAAAGGATATAAACAGTCACTTCTCAAAAGAAGACAT
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ilarity 52.3%;
Conservative
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52.3%;
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Pred. No. 0.5;
0; Mismatches
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OF DETECTION AND USES THEREOF
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US-09-596-002-15
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; ORGANISM: M.catarrhalis
US-09-540-236-1642
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SEQ ID NO 15
LENGTH: 28626
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Patent No. 6673910
GENERAL INFORMATION:
                                                                                                                                                          Query Match
Best Local Similarity
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Patent No. 6632636
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Best Local Similarity
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APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
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                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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18032 ATAATAAATTTGCCTCTAGTGTATCATGCCCTTGATC 18068
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                                  341 GIGGTCAGTTTCCATCAGGTGGATTATACCTTTGACC 377
                                                                                                      281 CAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACC 340
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                                                                     TTGCTTGGCACATCTCATAAGTGCGTGCATCAGCTGGCAGACCTA 18031
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Pred. No. 5.1;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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                                                                                              US-09-949-016-12028
                                                                                                                                                               SOFTWARE: FASTSEQ
SEQ ID NO 12028
LENGTH: 32043
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: APPLICANT: VENTER, J.
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    Matches
                          Best Local Similarity
                                             Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08 NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                            TYPE:
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                                                                                                                      ORGANISM: Human
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52.3%;
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Pred. No. 5.
  Mismatches
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                                             DB 4;
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184 GTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCAT 243

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RESULT 23
US-09-949-016-17033/c
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US-09-949-016-17032
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Best Local Similarity
Matches 97; Conser
                                                                                                    GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                        Sequence 17033, Application US/09949016 Patent No. 6812339
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Patent No. 6812339
GENERAL INFORMATION:
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SEQ ID NO 17032
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001107
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
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Pred. No. 21;
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                 RESULT 25
US-09-167-109-3
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 Sequence 3, Application US/09167109
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RESULT 24
US-09-248-796A-11532
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LENGTH: 194937
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAY
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
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SEQ ID NO 11532
LENGTH: 603
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Best Local
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Candida albicans
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                                                                                 369 AGCAACAAAAGAAACTGTTAGTGAACTTTTTGAAAATCAATGTCAGAATTGTTTTGGACT
                                                                                                                     189 CCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGC
                                                                                                                                                                 309 TGATATACAACAAAATGAGTTÄAGCGAAAGCGATTCAAGTGÄAÄATGATTTAAGÄGAAAT
                                                                                                                                                                                                         129 TAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 ATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACC 190
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                                                                                                                                                                                                                                                                         Similarity
                                       TGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGA 285
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TGGTCATGATTCATATGAATGTTCACTGGCATTTAGA 465
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48.7%;
                                                                                                                                                                                                                                                 Score 35.4; D
Pred. No. 0.9;
0; Mismatches
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Pred. No. 21;
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Patent No. 6399297

INFORMATION:

TRAF EXPRESSION

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; LOCATION: (218)..(1924);
; PUBLICATION INFORMATION;
; DATABASE ACCESSION NUMBER: U21092;
; DATABASE ENTRY DATE: 1995-03-23
US-09-167-109-3
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US-09-949-016-468
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APPLICANT: Cowsert, Lex M.
APPLICANT: Monia, Brett P.
APPLICANT: Xu, Xiaoxing S.
TITLE OF INVENTION: ANTISENSE MODULATION OF TR
FILE REFERENCE: ISPH-0321
CURRENT APPLICATION NUMBER: US/09/167,109
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 228
                                                                                                                                                                             US-09-949-016-468
                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 2000-10-20
                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 468
LENGTH: 2455
                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 468, Application US/09949016 Patent No. 6812339
                                                                                                           Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Human
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ORGANISM: Homo sapiens
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                                    72 TTCAGGCACAAAAGAACTCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAA 131
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TTGAGAGACAAAAGGAAATGCTTCGAAATAATGAATCCAAAATCCTTCATTTACAGCGAG 1181
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                                                                                                        5.9%;
                                                                                                                                                                                                                                                                                                             207012
                                                                                  Score 35.4; DB Pred. No. 2.1; 0; Mismatches
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Pred. No. 2.1;
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                                                                                                                             DB 4; Length 2455;
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US-09-949-016-4366
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; ORGANISM: Human US-09-949-016-4366
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                                                                  SOFTWARE: Fast
SEQ ID NO 4366
LENGTH: 7571
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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LENGTH: 2455
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Patent No. 6822070
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APPLICANT: Cleary, Alleen
TITLE OF INVENTION: Truncated Craf-1 Inhibits CD40 Signalling
FILE REFERENCE: 0575/50659
FILE REPERENCE: 0575/50659
CURRENT APPLICATION NUMBER: US/08/813,323C
CURRENT FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.1
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APPLICANT: Cheng, Ger
APPLICANT: Ye, Zheng-
                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILLING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILLING DATE: 2000-09-08
                                                                                                                                               NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo Sapiens
                                                TYPE: DNA
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                                                                                                                     FastSEQ for Windows Version
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Ye, Zheng-Sheng
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; LOCATION: 8083
; OTHER INFORMATION: a;
US-09-976-594-725
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US-09-976-594-725
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                                                RESULT 30
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   Sequence 32, Application US/09566921 Patent No. 6682888
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Best Local
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LENGTH: 8146
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Best Local Similarity
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
FILE REFERENCE: PA-0041 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Furness, Michael APPLICANT: Buchbinder, Jen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Incyte ID No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                                                                                           GAAGAGAAGAAGGAAGTGAAAAAGGAAAGAAAACCCAAAAAAAGAAATTAAGAAG 2381
                                                                                                                    TATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAG 316
                                                                                                                                                                                AAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTT 259
                                                                                                                                                                                                              ACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAG 199
                                                                                                                                                                                                                                                                         CCAAAGAAAGAAGTGGCTAAAAAGGAGGACAAAACACCTATCAAGAAGGAGGAAAAAACCA 2204
                                                                                                                                                                                                                                                                                                   CAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGAC 139
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                                                                                                                                                    TATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09976594
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46.8%;
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Pred. No. 4.
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Pred. No. 4.1;
0; Mismatches 126;
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                                                                                                                                                                                                                                                                                                                                   Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                               DB 4;
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                             US-09-949-016-16108
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16108, Ap
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                        ORGANISM: Human
                                                                                                                      TYPE: DNA
                                                                                                                                    ENGTH:
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                                                                                                                                    101300
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 16108
                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 11917
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6682888 475473.1
NAME/KEY: unsure
LOCATION: 9384, 10290-10321, 10325
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(101300)
OTHER INFORMATION: n = A,T,C
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Pred. No. 5.4;
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OF DETECTION
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Score 35.4;

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Length 101300;

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US-09-949-016-17590
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Wiedler, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Serill Reference: 38-10(15849)B
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: 05/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION UNBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 17590
LENGTH: 247299
                                                                                                                                                                                                             Sequence 8128, Applic Patent No. 6833447 GENERAL INFORMATION:
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 GCTCTACAGAGTGACCAGGGAGTACACCCCAAAACAAGAAGGAGGCAGAGAAGATCATCAA
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sec
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION UNMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
INUMBER OF SEQ ID NOS: 16825
SEQ ID NO 832
LENGTH: 8352
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US-09-902-540-832/c
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SEQ ID NO 8128
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 832, Application US/09902540 Patent No. 6833447
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Best Local Similarity
                                                                                                                                                                                                                                                                            Matches
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TYPE: DNA
ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                   4490
                                                                                                                                                                                                      4610 GAGAAGCTCTACGAGCTGATGCAGGTGAGATCGAGATTCTCCAGGTGGAGAAGAAGATC
4430 ATTG 4427
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                                                                                                                                                                      209 GAGAAGATCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAAT 268
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                                 329 CTTG 332
                                                                                                269 AATCAGTTTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAGTTCATCAG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                736 ATGCAGGCCATTCAGAAGGAGCTGGGTGAGCGCGACGAGTTCAAGAACGAGATTCAGGAG
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                                                                                                                                       CGCACGCGCGTCAAGAAGCAGATGGAGAAGACCCAGAAGGAGTACTACCTGAATGAGCAG
                                                                   ATGCAGGCCATTCAGAAGGAGCTGGGTGAGCGCGACGAGTTCAAGAACGAGATTCAGGAG
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Pred. No. 2.4;
0; Mismatches
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Pred. No. 5;
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RESULT 35 US-09-949-016-13146

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US-09-949-016-194263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                             Query Match
Best Local Similarity
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SEQ ID NO 13146
LENGTH: 58829
                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 194263
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/237,768 PRIOR FILING DATE: 2000-10-03
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CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: VENTER, J.
                                                                                                                                                                                                 TYPE: DNA
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LOCATION: (1)...(58829)
OTHER INFORMATION: n = A,T,C or G
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  TGTCTATATTTATATCTAACATCAGGGCTCCCAGATATATAAAGCAAATATGGAGAGAAG
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                                   TGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGG 152
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                                                                                 Conservative
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                                                                          Score 35; DB 4;
Pred. No. 1.2;
0; Mismatches 10
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Pred. No. 16;
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OF DETECTION AND USES THEREOF
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US-09-949-016-14033/c
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; ORGANISM: Human
US-09-949-016-17262
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
             Sequence 14033, Application US/09949016
PATENT NO. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
FILE REFERENCE: CLU01307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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Best Local Similarity
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TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version
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PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                                                                                                                              273 AGTTTAATCAAGATG 287
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Pred. No. 11;
0; Mismatches 10
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RESULT 40
US-09-949-016-205411/c
US-09-949-016-205411, Application US/09949016
; Sequence 205411, Application US/09949016
; Patent NO. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
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; OTHER INFORMATION: n = A,T,C or US-09-949-016-14033
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; Sequence 205410, Application US/09949016
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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Best Local S
Matches 56
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Best Local S
Matches 60
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 205410
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
-09-949-016-205410
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                  CATGYATAGCACTTTTTGATGGTAAACTTGAGGAAGACATTT 264
                                                                                                                                                                                                                                        CAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTT 322
                                                                                                                                                                                                                                                                                   AAGGACACCATCAAGAAAGTGAAAAGACGGCCCACAAGTTGGAAGAAAATACTTGCAAAT
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       Score 34.8; DB 4; Length 601; Pred. No. 1.4; Indels
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    KNOWN GENES
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    ASSOCIATED
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OF DETECTION AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
VIMMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 205411
LENGTH: 601
TYPE: DNA
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                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Window
SEQ ID NO 17549
LENGTH: 24345
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                                                                                                                                                                                    Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/231,498 PRIOR FILING DATE: 2000-09-08
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                                                                                                                                                                                                                                                                    ORGANISM: Human
                                                                                                                                                                                                                                                                                            TYPE: DNA
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Local Similarity 58.8%;
                                                                                13643 AAGGACCATCAAGAAAGTGAAAAGACGGCCCACAAGTTGGAAGAAAATACTTGCAAAT 13702
                                    281 CAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTT 322
                                                                                                                   221 AAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAAT 280
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                                                                                                                                                                                                                                                                                                                                                         Version
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Pred. No. 13;
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Pred. No. 1.4;
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13744
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RESULT 42 US-09-908-988B-5

Sequence 5, Application US/09908988B Patent No. 6740751

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RESULT 43
US-09-248-796A-80
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                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/248,796A CURRENT FILING DATE: 1999-02-12 PRIOR APPLICATION NUMBER: US 60/074,725 PRIOR ETLING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: US 60/096,409 PRIOR FILING DATE: 1998-08-13 NUMBER OF SEQ ID NOS: 28208 SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 80, Application US/09248796A Patent No. 6747137
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SEQ ID NO 5
LENGTH: 1597
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APPLICANT: SPENCER, JEFFREY A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
TITLE OF INVENTION: IN STRIATED MUSCLE CELLS
FILE REFERENCE: MYOG:028US
CURRENT APPLICATION NUMBER: US/09/908,988B
CURRENT FILING DATE: 2000-07-18
CURRENT FILING DATE: 2000-07-18
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                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                          LENGTH: 672
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LOCATION: (29)
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                                         172
566 GGTATCAACAAAATGTTGGATGAAGAGA 593
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                                       AAAAACGCCGAAAAGTATCACTTGGAGGAATATAAACAAAATTTTATCGAACAATTGAAT
                                                                                                                    ATTGATAAGGCATATGTATTAGTTGAACATAAATTTCAAGAATTATGGGAAAATGCATCG
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                                                                            TTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGAT
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52.0%;
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Pred. No. 2;
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 430
LENGTH: 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6812339
                                                                         Matches
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Best Local
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Best Local S
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APPLICANT: Secriet, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 67595
                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Lodes, Michael APPLICANT: Mohamath, Rao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                 ORGANISM: Human
                                                                                                                                                                                    TYPE: DNA
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                                   158 GATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATC
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                                                                                         Similarity
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Pred. No. 2;
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                                                                                                           DB 4;
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                                                                       41;
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                                                                                                           Length 2349;
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                     is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.
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:/cgn2_6/ptodata/2/pubpna/US10P_PUBCOMB.seq:*
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19 US-10-087-192-3207
10 US-10-040-862-3207
10 US-10-057-475B-2801
10 US-10-154-884B-3207
10 US-10-154-884B-3207
10 US-10-154-884B-3207
10 US-10-154-884B-3207
10 US-10-154-884B-5724
10 US-10-164-862-2801
10 US-10-164-862-5724
11 US-10-057-475B-5724
12 US-10-057-475B-5724
13 US-10-057-475B-5724
14 US-10-057-475B-5724
15 US-10-057-475B-5724
16 US-10-057-475B-5724
17 US-10-057-475B-5724
18 US-10-094-466-43
18 US-10-29-386-25411
19 US-10-044-466-43
10 US-10-044-466-43
10 US-10-044-466-43
11 US-10-044-466-43
11 US-10-044-466-43
12 US-10-046-692-4917
13 US-10-057-475B-4917
14 US-10-191-803-331-67
15 US-10-29-386-9211
16 US-10-29-386-9211
17 US-10-057-475B-4917
18 US-10-29-386-921
19 US-10-29-386-921
10 US-10-28-92-38
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Sequence 39, Appl
Sequence 493, App
Sequence 493, App
Sequence 3207, Ap
Sequence 3207, Ap
Sequence 3207, Ap
Sequence 3207, Ap
Sequence 2801, Ap
Sequence 2801, Ap
Sequence 2801, Ap
Sequence 2801, Ap
Sequence 5724, Ap
Sequence 572
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Sequence 1, Application US/10627571

| Replication No. US20040082771A1
| GENERAL INFORMATION:
| APPLICANT: KASID, Usha N. |
| APPLICANT: KOMAR, Deepak |
| APPLICANT: KUMAR, Deepak |
| APPLICANT: AHMAD, IMXAR |
| APPLICANT: AHMAD, IMXAR |
| CURRENT FILLE OF INVENTION NUMBER: US/10/627,571 |
| CURRENT APPLICATION NUMBER: US/10/627,571 |
| CURRENT APPLICATION NUMBER: US 60/264,062 |
| PRIOR APPLICATION NUMBER: US 60/264,062 |
| PRIOR APPLICATION NUMBER: PCT/US02/02212 |
| PRIOR FILING DATE: 2001-01-26 |
| PRIOR FILING DATE: 2002-01-28 |
| NUMBER OF SEQ ID NOS: 25 |
| SOFTWARE: PatentIn version 3.2 |
| SEQ ID NO 1 |
| LENGTH: 1915 |
| TYPE: DNA |
| ORGANISM: Homo sapiens |
| PRIOR FILING DATE: DOS |
| ORGANISM: Homo sapiens |
| PRIOR FILING DATE: DOS |
| ORGANISM: Homo sapiens |
| PRIOR FILING DATE: DOS 
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; NAME/KEY: misc feature
; OTHER INFORMATION: SCC-S2
US-10-627-571-1
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US-10-627-571-1
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Best Local Similarity 100.
Matches 601; Conservative
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                         GGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGT
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GGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAGT
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3 US-10-087-192-1105
10 US-10-425-115-137599
10 US-10-335-977-3199
18 US-10-335-977-3200
18 US-10-672-787-15
10 US-09-880-107-2380
21 US-10-741-600-17795
22 US-10-741-601-18684
23 US-09-864-761-19684
24 US-09-864-761-1935
25 US-10-719-993-7050
26 US-10-719-993-7650
27 US-10-719-993-6864
28 US-10-719-993-6864
29 US-10-719-993-6864
20 US-10-741-601-5611
20 US-10-087-192-2002
21 US-10-087-192-23404
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Pred. No. 3.9e-169;
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                                                                                                                                                                                                                                                                                                                                                                                              Length 1915;
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Sequence 11759, Ap
Sequence 31759, Ap
Sequence 3199, Ap
Sequence 3200, Ap
Sequence 2380, Ap
Sequence 17795, A
Sequence 117795, A
Sequence 103224,
Sequence 10325, Ap
Sequence 7050, App
Sequence 7050, Ap
Sequence 1935, Ap
Sequence 5611, App
Sequence 5611, App
Sequence 5611, App
Sequence 119, App
Sequence 111, Appl
Sequence 115, App
Sequence 115, App
Sequence 116, App
Sequence 117, Appl
Sequence 118, Appl
Sequence 23404, Ap
Sequence 23404, Ap
Sequence 4, Appli
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                                     240
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                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: human TNF-induced ; OTHER INFORMATION: complete CDS US-10-491-545A-48
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SEQ ID NO 48
; LENGTH: 1892
; TYPE: DNA
ORGANISM: Homo sapiens
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US-10-491-545A-48
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APPLICANT: Li, Congfen
APPLICANT: Li, Congfen
APPLICANT: Li, Congfen
APPLICANT: Li, Congfen
APPLICANT: Masuda, Esteban
APPLICANT: Pardo, Jorge
APPLICANT: Pardo, Jorge
APPLICANT: Rigel Pharmaceuticals, Inc.
TITLE OF INVENTION: Modulators of Lymphocyte Activation and Migration
FILE REFERENCE: 021044-00330US
CURRENT APPLICATION NUMBER: US/10/491,545A
CURRENT FILING DATE: 2004-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48, Ap
Publication No.
                                                                                                                                                                                           Matches 600;
                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/327,212
PRIOR FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: WO PCT/US02/31618
PRIOR FILING DATE: 2002-10-02
NUMBER OF SEQ ID NOS: 96
                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                     Local Similarity
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                                            60 AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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No. US20050130117A1
                                                                                                                                                                                           97.9%;
milarity 99.7%;
Conservative
                                                                                                                                                                                         Score 588.4; DB 22;
Pred. No. 2.3e-165;
Pred. No. 2.3e-165;
                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                     Length 1892;
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CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: C0/070,923
PRIOR APPLICATION NUMBER: C0/070,923
PRIOR APPLICATION NUMBER: C0/070,923
PRIOR APPLICATION NUMBER: C0/068,007
PRIOR APPLICATION NUMBER: C0/068,007
PRIOR FILING DATE: 1997-12-18
PRIOR PRILING DATE: 1997-12-19
PRIOR PRILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: C0/068,369
PRIOR PILLING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: C0/068,368
PRIOR PILLING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: C0/068,068
PRIOR APPLICATION NUMBER: C0/068,063
PRIOR APPLICATION NUMBER: C0/068,064
PRIOR PILLING DATE: 1997-12-18
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Publication No. US20030055236A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: 110 Human Secreted Proteins
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; LOCATION: (1934)
; OTHER INFORMATION:
US-10-097-065-98
      Sequence 98, Applica Publication No. US20 GENERAL INFORMATION:
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PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 98
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LOCATION: (1926)
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RESULT 3 US-10-097-065-98

GENERAL INFORMATION:

APPLICANT: Moore, REFERENCE:

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CURRENT APPLICATION NUMBER: US/10/372,876

CURRENT FILING DATE: 2003-02-26

PRIOR APPLICATION NUMBER: 09/334,595

PRIOR PFLLING DATE: 1999-06-17

PRIOR PFLLING DATE: 1998-12-17

PRIOR PFLLING DATE: 1998-12-17

PRIOR PFLLING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR APPLICATION NUMBER: 60/068,007

PRIOR PFLLING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/068,057

PRIOR PFLLING DATE: 1997-12-18

PRIOR PFLLING DATE: 1997-12-18

PRIOR APPLICATION NUMBER: 60/068,066

PRIOR PILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,369

PRIOR PILING DATE: 1997-12-19

PRIOR PILING DATE: 1997-12-19

PRIOR PILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,367

PRIOR PILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,369

PRIOR PILING DATE: 1997-12-19

PRIOR APPLICATION NUMBER: 60/068,369

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Matches 590; Conserv
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LOCATION: (1934)
OTHER INFORMATION: n e
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LOCATION: (1926)
OTHER INFORMATION:
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LOCATION: (1928)
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OTHER INFORMATION:
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Pred. No. 2.7e-165;
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Sequence 215, Application US/10755889
Publication No. US20040171823A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
ITILE OF INVENTION: POLYNUCLEOTIDES AND POLY
TITLE OF INVENTION: PATHWAY
FILE REFERENCE: D0244 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR PILING DATE: 2003-05-12
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; ORGANISM: Homo sapiens
US-10-755-889-215
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US-10-755-889-215
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SEQ ID NO 215
LENGTH: 1814
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Best Local Similarity
Matches 565; Conserv
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TGACCGTGGTCAGTTTCCAGCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGC 395
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nilarity 99.8%;
Conservative
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Pred. No. 3.6e-158;
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RESULT 6
US-10-755-889-217
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CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
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Best Local Similarity
Matches 565; Conserv
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SEQ ID NO 217
LENGTH: 2003
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ORGANISM: Homo
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 CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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APPLICANT: MORIS, DAVID W.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2000-103-02
NUMBER OF SEQ ID NOS: 2059
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-087-192-497
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US-10-087-192-497
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Best Local Similarity 99.8%;
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                                                        CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTTGTGAATTTTTTGGCTGCCT
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Pred. No. 3.9e-158;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR FILING DATE: 2003-01-14
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR FILING DATE: 2003-05-12
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin version 3.2
SEQ ID NO 39
LENGTH: 2081
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US-10-755-889-39
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Best Local Simi
Matches 565;
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CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
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AAATGTTGGATGAAGAGAACATATGA
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No. US20040171823A1
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Pred. No. 4e-158;
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 496
LENGTH: 58723
TYPE: DNA
ORGANISM: Homo sapiens
US-10-087-192-496
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US-10-087-192-496
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publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
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Best Local Similarity 99.8%;
Matches 565; Conservative
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Pred. No. 3e-157;
0; Mismatches 1;
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 22914
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Best Local :
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
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PEATURE:

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN FETALUB 2.60e-01

OTHER INFORMATION: NT HIT: 917657123, EVALUE 0.00e+00

OTHER INFORMATION: NT HIT: 917657123, EVALUE 0.00e+00
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ORGANISM: Homo sapiens
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AAAT 544
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                                                                                             TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
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                                                                                                                                              CACATGGACGGGTTAATAATGTGTTTTGATCATTTTTCAGATTGTGAATTTTTGGCTGCCT
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Pred. No. 7.1e-152;
D; Mismatches 1;
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US-10-087-192-493
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CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
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Best Local S
Matches 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 493
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                     TATCAACAAAATGTTGGATGAAGAGAACATATGA
                                                                                             GGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGG
                                                                                                                                                                TGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAACTTTTT
                                                                                                                                                                                                                     GTCCAGGCTGCTGAACGAGTGCCGAGAGCTCCTACACGAGATCATTCAGCGCCACCTTAC
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                                                                      GGCTGCCTTGTACAATCCCTTTGGAAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGG
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o. US20020182586A1
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86.1%;
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Pred. No. 1.1e-121;
0; Mismatches 80;
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RESULT 12
US-10-087-192-494
; Sequence 494, Applicat
; Publication No. US2000
; Publication No. US2000;
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-03-01
FRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 494
LENGTH: 2087
TYPE: DNA
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US-10-087-192-494
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Best Local Similarity
Matches 490; Conserv
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
1048
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 AAATGTTGGATGAAGAGAACATATGA 1073
                        AAATGTTGGATGAAGAGAACATATGA
                                                                                                                                     CTCACGGACGGGTTAATAATGTCTTTGACCATTTTTCAGATTGTGATTTTTTGGCTGCCT
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                                                                TGTACAATCCCTTTGGAAAGTTTAAACCTCACTTACAGAAACTTTGCGACGGCATCAACA
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Pred. No. 4.2e-122;
0; Mismatches 76;
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RESULT 13 US-09-796-692-3207

RESULT 14
US-10-040-862-3207
; Sequence 3207, Application US/10040862
; Publication No. US20030078396A1
; GENERAL INFORMATION:

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GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Gaiger, Alexander

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR APPLICATION NUMBER: 60/200,545
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PRIOR APPLICATION NUMBER: 60/200,303

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/200,779

PRIOR APPLICATION NUMBER: 60/200,999

PRIOR FILING DATE: 2000-05-01

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR APPLICATION NUMBER: 60/202,084

PRIOR FILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

PRIOR FILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-04

PRIOR PILING DATE: 2000-05-05

PRIOR PILING DATE: 2000-05-07

PRIOR PILING DATE: 2000-05-07
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SOFTWARE: PastSEQ for Windows Version
SEQ ID NO 3207
LENGTH: 287
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Best Local Similarity
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PRIOR FILING DATE: 2000-08-07
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OR FILING DATE: 2000-07-14
OR PPLICATION NUMBER: 60/222,903
OR FILING DATE: 2000-08-03
OR APPLICATION NUMBER: 60/223,416
OR FILING DATE: 2000-08-04
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                           CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTT
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99.7%;
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Pred. No. 6.7e-75;
0; Mismatches 1;
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US-10-057-475B-3207
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; Publication No. US20040002068A1
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; ORGANISM: Homo
US-10-040-862-3207
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Best Local Similarity
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SEQ ID NO 3207
LENGTH: 287
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Hematological Malignancies
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PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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FILING DATE: 2000-05-04
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FILING DATE: 2000-04-27
APPLICATION NUMBER: US 60/200,303
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Algate, Paul A
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Retter, Marc
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Pred. No. 6.7e-75;
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RESULT 16
US-10-154-884B-3207
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-057-475B-3207
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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Best Local Similarity
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APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
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CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2022-01-22
PRIOR APPLICATION NUMBER: US 60/186,126
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APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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FILING DATE: 2000-04-28
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Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
                                                            TTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGTTTTGATCATTTTT
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Algate, Paul A
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Clapper, Jonathan
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Pred. No. 6.7e-75;
0; Mismatches 1
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RESULT 17
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; ORGANISM: Homo sapiens
US-10-154-884B-3207
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Sequence 3207, Application US/10764324
Publication No. US20040175739A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 3207
LENGTH: 287
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Matches 286; Conserv
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CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Hematological Malignancies
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OR APPLICATION NUMBER: US 60/200,303
IOR FILING DATE: 2000-04-28
IOR APPLICATION NUMBER: US 60/200,779
IOR FILING DATE: 2000-04-28
IOR APPLICATION NUMBER: US 60/200,999
IOR APPLICATION NUMBER: US 60/200,999
IOR FILING DATE: 2000-05-01
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Retter, Marc W.
Corixa Corporation
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99.7%;
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RESULT 18
US-09-796-692-2801/c
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SEQ ID NO 3207
LENGTH: 287
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PRIOR FILING DATE: 2000-04-28
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
                                                                                                                                                          Sequence 2801, Application US/09796692 Publication No. US20020198362A1 GENERAL INFORMATION:
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Best Local (
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mandion, Jane
APPLICANT: MARNION, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077, 001200
CURRENT APPLICATION NUMBER: US/09/796,692
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TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR PILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US/60/186,126
PRIOR APPLICATION NUMBER: US/60/186,126
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PRIOR FILLING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILLING DATE: 2000-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/218,950 PRIOR FILING DATE: 2000-07-14
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PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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nes 286; Conserv
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99.7%;
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Pred. No. 6.7e-75;
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THERAPY

CURRENT FILING

DATE:

2001-03-01

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Sequence 2801, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Hematological Malig
FILE REFERENCE: 014058-013520US
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US-10-040-862-2801/c
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; ORGANISM: Homo sapiens
US-09-796-692-2801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.2
Best Local Similarity 99.3
Matches 285; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 2801
LENGTH: 287
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PRIOR FILING DATE: 2000-08-07
NUMBER OF COLUMBER OF C
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
CURRENT APPLICATION NUMBER: US/10/040,862
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APPLICATION NUMBER:
FILING DATE: 2000-05
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APPLICATION NUMBER: 60/200,303
FILING DATE: 2000-04-28
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Pred. No. 2e-74;
                                                                                    and Methods for the Detection, al Malignancies
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                                                                                                                Diagnosis and
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                                                                                                                Therap
                                                                                                      ; Sequence 2801, Application US/10057475B; Publication No. US20040002068A1; GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander; APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane

APPLICANT: Clapper, Jonathan David APPLICANT: Wang, Aljun

APPLICANT: Wang, Aljun
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US-10-057-475B-2801/c
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                            APPLICANT:
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Ordonez, Nadia Carter, Lauren McNeill, Patricia Dianne Corixa Corporation

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-2801
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Best Local :
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SOFTWARE: FastSEQ for
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OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,779
OR FILING DATE: 2000-04-28
OR APPLICATION NUMBER: US 60/200,999
OR FILING DATE: 2000-05-01
OR APPLICATION NUMBER: US 60/202,084
OR FILING DATE: 2000-05-04
OR APPLICATION NUMBER: US 60/206,201
OR FILING DATE: 2000-05-22
OR APPLICATION NUMBER: US 60/218,950
OR APPLICATION NUMBER: US 60/218,950
OR APPLICATION NUMBER: US 60/222,903
OR FILING DATE: 2000-08-03
OR FILING DATE: 2000-08-03
OR FILING DATE: 2000-08-03
OR FILING DATE: 2000-08-03
OR PELICATION NUMBER: US 60/222,903
OR PELICATION NUMBER: US 60/233,416
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                                         492 CAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTT 538
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US-10-154-884B-2801/c
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                                                                                                                                                                          Sequence 2801, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2801
LENGTH: 287
        APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Metter, Marc W.
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TIPLE OF INVENTION: Compositions and Methods for the Detection,
TIPLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
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Best Local Similarity
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PRIOR PILING DATE: 2000-03-01
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR PILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
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CURRENT FILING DATE: 2002-01-22
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CURRENT APPLICATION NUMBER: US/10/154,884B
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APPLICATION NUMBER: US 60/200,303
FILING DATE: 2000-04-28
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FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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APPLICATION NUMBER: US 60/218,950
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Pred. No. 2e-74;
0; Mismatches
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RESULT 22
US-10-764-324-2801/c
; Sequence 2801, Application US/10764324
; Publication No. US20040175739A1
; GENERAL INFORMATION:
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Matches
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LENGTH: 287
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Method, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
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PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
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PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
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APPLICATION NUMBER: US 60/206,201
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PRIOR APPLICATION NUMBER: US/10/040,862
PRIOR FILING DATE: 2001-11-06
APPLICATION NUMBER: US 60/186,126
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GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Algate, Faul A,

APPLICANT: Algate, Faul A,

APPLICANT: Mannion, Jane

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

FILE REFERENCE: 2077.001200

CURRENT APPLICATION NUMBER: US/09/796,692

CURRENT FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: 60/186,126

PRIOR APPLICATION NUMBER: 60/190,479

PRIOR FILING DATE: 2000-03-17

PRIOR APPLICATION NUMBER: 60/200,545

PRIOR FILING DATE: 2000-04-27

PRIOR FILING DATE: 2000-04-27
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US-09-796-692-5724
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Best Local Similarity
Matches 285; Conserv
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LENGTH: 287
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
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ORGANISM: Homo sapiens
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APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,999
                         APPLICATION NUMBER: 60/200,303 FILING DATE: 2000-04-28
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99.3%;
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US-10-040-862-5724
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               GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap:
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/60/1066
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                     Sequence 5724, Application US/10040862
Publication No. US20030078396A1
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PRIOR APPLICATION NUMBER: US 60/190,479
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; OTHER INFORMATION: n=A,T,C
US-09-796-692-5724
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Best Local Similarity
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SEQ ID NO 5724
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TYPE: SM.
ORGANISM: HOMO SAPIENS
PEATURE:
RAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n=A,T,C o
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FILLING DATE: 2000-08-03
APPLICATION NUMBER: 60/223,416
FILING DATE: 2000-08-04
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APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
FILING DATE: 2000-05-04
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APPLICATION NUMBER: 60/223,378
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                       491 TCAGATTGTGAATTTTTGGCCTGCCTTGTATAATCCTTTTTGGGAATTTTT
                                                                                                      431 ATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTT
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TCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTTGGGAATTTT
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DS: 9597
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98.6%;
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Pred. No. 5.4e~71;
0; Mismatches 3;
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 288
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PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PRIOR PRIOR DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/222,903
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR APPLICATION NUMBER: US 60/223,416
PRIOR PRIOR PRIOR DATE: 2000-08-04
PRIOR PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR PRIOR DATE: 2001-03-01
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FASTSEQ for Windows Version 3.(
SEQ ID NO 5724
LENGTH: 288
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US-10-057-475B-5724
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Sequence 5724, Application US/10057475B
Publication No. US20040002068A1
GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Clapper, Jonathan David
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Best Local Similarity
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NAME/KEY: unsure
LOCATION: (59)
OTHER INFORWATION: n=A,T,C
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NAME/KEY: unsure
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TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: n=A,T,C
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FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
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APPLICATION NUMBER: US 60/200,303
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Conservative
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Pred. No. 5.4e-71;
0; Mismatches 3
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SOFTWARE: FastSEQ for Windows Version 3.

SEQ ID NO 5724
LENGTH: 288
TYPB: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(288)
RESULT 26
US-10-154-884B-5724
; Sequence 5724, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-03-01
PRIOR PEPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-28
PRIOR PEPLICATION NUMBER: US 60/200,709
PRIOR PEPLICATION NUMBER: US 60/200,779
PRIOR PEPLICATION NUMBER: US 60/200,779
PRIOR PELICATION NUMBER: US 60/200,779
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR PELICATION NUMBER: US 60/200,999
PRIOR PELICATION NUMBER: US 60/202,084
PRIOR PEPLICATION NUMBER: US 60/206,201
PRIOR PEPLICATION NUMBER: US 60/206,201
PRIOR PEPLICATION NUMBER: US 60/206,201
PRIOR PEPLICATION NUMBER: US 60/208,201
PRIOR PEPLICATION NUMBER: US 60/208,201
PRIOR PEPLICATION NUMBER: US 60/208,203
PRIOR PEPLICATION NUMBER: US 60/208,203
PRIOR PEPLICATION NUMBER: US 60/218,950
PRIOR PEPLICATION NUMBER: US 60/222,903
PRIOR PELICATION NUMBER: US 60/222,903
PRIOR PELICATION NUMBER: US 60/222,903
PRIOR PELICATION NUMBER: US 60/222,903
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Matches 284
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
TILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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Ordonez, Nadia
Carter, Lauren
McNeill, Patricia Dianne
Corixa Corporation
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Pred. No. 5.4e~71;
0; Mismatches 3;
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RESULT 27
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; LOCATION: (1)...(288)
; OTHER INFORMATION: n = g,
US-10-154-884B-5724
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Sequence 5724, Application US/10764324 Publication No. US20040175739A1 GENERAL INFORMATION:
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PRIOR TILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
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CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
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APPLICANT: Corixa Corporation

TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis

TITLE OF INVENTION: Hematological Malignancies
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
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FILING DATE: 2000-04-28
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FILING DATE: 2000-04-28
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5724
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: unsure
LOCATION: (58)
OTHER INFORMATION: n=A,
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CURRENT APPLICATION NUMBER: US/10/764,324
CURRENT FILING DATE: 2004-01-23
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TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Hematological Malignancies
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APPLICANT: Algate, Paul A.
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APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
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Retter, Marc
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Pred. No. 5.4e-71;
0; Mismatches 3
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RESULT 29
US-10-094-466-41
; Sequence 41, Application US/10094466
; Publication No. US20030203363A1
; GENERAL INFORMATION:
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Best Local S
Matches 346
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CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers.
SEQ ID NO 25411
LENGTH: 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25411, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION:
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
APPLICANT: Spytek et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
FEATURE:
FEATURE:
OTHER INFORMATION: MAP TO AC012678.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.51
OTHER INFORMATION: SWISSPROT HIT: Q61768, EVALUE 1.10e-01
OTHER INFORMATION: NT HIT: AF120995.1, EVALUE 1.30e-01
OTHER INFORMATION: EST_HOMAN HIT: BF744133.1, EVALUE 2.006
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                                                                                                                                                                                          ATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAA
                                                                                                                                                                                                                                                                                   ATAGGAACGTGCTCCCAATCTCCTGCATGAGTGCAAGGACCTGGTGCATGAACTGGTGC
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                                                                                                                                                                                                                           AGCGGCACCTGACGCCCAGGACCCACGGGCGCATCAACCACGTCTTTAACCACTTTGCCG
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Pred. No. 2.5e-60;
0; Mismatches 181;
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 CTGACCGCCAAGTCCCACGGCCGCATCAACCACGTGTTCCGGCCACCTAGCCGACTGCGAC
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CURRENT APPLICATION NUMBER: US/10/094,460
CURRENT FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,281
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR PRILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/274,849
PRIOR FILING DATE: 2001-03-09
PRIOR PRILING DATE: 2001-03-09
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-03-12
PRIOR PRILING DATE: 2001-12-04
PRIOR PRILING DATE: 2001-12-04
PRIOR PRILING DATE: 2001-12-04
PRIOR PRILING DATE: 2001-12-04
PRIOR PRILING DATE: 2001-13-13
PRIOR PRILING DATE: 2001-13-13
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-13
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Best Local Similarity
Matches 347; Conserv
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ORGANISM: Homo |
FEATURE:
NAME/KEY: CDS
LOCATION: (26).
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Prior Application data removed -
NUMBER OF SEQ ID NOS: 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OR FILING DATE: 2001-03-13
OR APPLICATION NUMBER: 60/335,302
OR FILING DATE: 2001-10-31
OR APPLICATION NUMBER: 60/275,601
OR FILING DATE: 2001-03-13
OR APPLICATION NUMBER: 60/276,000
OR FILING DATE: 2001-03-14
OR APPLICATION NUMBER: 60/277,338
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CTCACTGCCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAA
                                                    GTGCTGGCCGGGCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCAC
                                                                                   GTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCAC
                                                                                                                                                                CGCTGCCTGGCCATGACGGCCGTCAGCTTCCACCAGGTGGACTTCACCTTCGACCGGCGC
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nilarity 59.9%;
Conservative
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Pred. No. 2.2e-51;
0; Mismatches 232;
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FEATURE:

NAME/KBY: misc feature

OTHER INFORMATION: Incyte ID No:
US-10-416-314-70
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US-10-416-314-70
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APPLICANT: KAREHT, Stephanie K.
TITLE OF INVENTION: SECRETED PROTEINS
FILE REFERENCE: PI-0287 USN
CURRENT APPLICATION NUMBER: US/10/416,314
CURRENT FILING DATE: 2003-05-08
PRIOR APPLICATION NUMBER: US 60/247,505
PRIOR FILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
Query Match
Best Local Similarity
Matches 347; Conserv
                                                                                                                                                                                                      SOFTWARE: PERL Program SEQ ID NO 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 70, Application US/10416314
Publication No. US20040082508A1
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                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/249,824
PRIOR FILING DATE: 2000-11-16
PRIOR APPLICATION NUMBER: US 60/252,824
PRIOR FILING DATE: 2000-11-21
                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 130
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                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                          LENGTH: 2108
                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 60/256,448
                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/254,305 FILING DATE: 2000-12-08
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WARREN, Bridget A.
HONCHELL, Cynthia D.
LU, Dyung Aina M.
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BAUGHN, Mariah R.
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ISON, Cra
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CHAWLA, Narinder K.
 Conservative
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                   34.6%;
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                 Score 207.8; DB 18; Pred. No. 4.4e-51;
 Mismatches
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                                                                            APPLICANT: Xue, Aidong J.
APPLICANT: Ma, Yunqing
APPLICANT: Mang, Zhiwei
APPLICANT: Zhang, Zhiwei
APPLICANT: Zhang, Zing A.
APPLICANT: Zhang, Jie
APPLICANT: Wanng, Jie
APPLICANT: Wanng, Jie
APPLICANT: Wanng, Jie
APPLICANT: Nounanac, Radoje T.
TITLE OF INVENTION: No. US20020150898A1el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791C1P2E
CURRENT APPLICATION NUMBER: US/09/816,828
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION UNMBER: 09/770,160
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/552,929
PRIOR FILING DATE: 2000-04-18
PRIOR FILING DATE: 2000-04-18
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US-09-816-828-5
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               SOFTWARE: pt_FL_genes
SEQ ID NO 5
LENGTH: 1188
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Patent No. US20020150898A1
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                                                                          NUMBER OF SEQ ID NOS:
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 TYPE: DNA
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US-09-816-828-5
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PRIOR APPLICATION NUMBER: 60/274, 281
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/288,148
PRIOR FILLING DATE: 2001-05-02
PRIOR PRIOR APPLICATION NUMBER: 60/274,849
PRIOR FILLING DATE: 2001-03-09
PRIOR PRIOR APPLICATION NUMBER: 60/275,235
PRIOR FILLING DATE: 2001-03-12
PRIOR FILLING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: 60/338,375
PRIOR FILLING DATE: 2001-12-04
                                                                                                                                                                                                                                                                                 Sequence 43, Application US/10094466
Publication No. US20030203363A1
GENERAL INFORMATION:
APPLICANT: Spytek et al.
TITLE OF INVENTION: NOVEL HUMAN PROTEINS,
TITLE OF INVENTION: AND METHODS OF USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-230D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/094,466
CURRENT FILING DATE: 2002-03-07
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Pred. No. 1.4e-50;
0; Mismatches 229;
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; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)...(566)

US-10-094-466-43
                   RESULT 33
US-10-764-420-2116
; Sequence 2116, Application US/10764420
; Publication No. US20050084872A1
; GENERAL INFORMATION:
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PRIOR PILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/335,302
PRIOR FILING DATE: 2001-0-31
PRIOR FILING DATE: 2001-03-13
PRIOR PILING DATE: 2001-03-13
PRIOR APPLICATION NUMBER: 60/275,601
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/277,338
PRIOR FILING DATE: 2001-03-03
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-09
PRIOR PRIOR FILING DATE: 2001-03-09
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/277,338
PRIOR FILING DATE: 2001-03-14
PRIOR PR
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Best Local Similarity
Matches 339; Conserv
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TYPE: DNA
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GACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGCT
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CTACGGCCCGCGAGCCCTACCGCTCCCACCTGCGCAGGATCTGCGAGGGCCTGGGGCCG
                                                GTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACAA
                                                                                                   CCACGGCCGCATCAACCACGTGTTCGGCCACCTAGCCGACTGCGACTTCCTGGCTGCGCT
                                                                                                                                                                                                          GCTGCTCGAGTGCCGCGACCTGCTGCACCAGGCCGTGGGTCCCCACCTGACCGCCAAGTC
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APPLICANT: Tan, Yejun
APPLICANT: Dai, Hongyue
TITLE OF INVENTION: Methods For Determining Whether An Agent
TITLE OF INVENTION: Possesses A Defined Biological Activity
FILE REFERENCE: ROSA122057
CURRENT APPLICATION NUMBER: US/10/764,420
CURRENT FILING DATE: 2004-01-23
PRIOR APPLICATION NUMBER: US 60/442,797
PRIOR PILING DATE: 2003-01-24
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 3683
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2116
LENGTH: 1389
TYPE: DNA
ORGANISM: Mus musculus
FEAUTRE:
NAME/KEY: misc_feature
1.0CATTON: 80
                                               RESULT 34
US-09-822-849A-81
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Sequence 81, Application US/09822849A Patent No. US20020045170A1 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                TGTTGGATGAAGAGAACATATGA 601
                                                                                                                                                                               ACAGCCCAGCAGAGCCCTACCGGAGCCATCTGTGCCGCATCTGTGATGGCCTCGGGAGGA
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Pred. No. 8.6e-49;
D; Mismatches 227;
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; LENGTH: 1113
; TYPE: DNA
; ORGANISM: Homo :
US-09-822-849A-81
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TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING
FILE REFERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/195,582
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
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Best Local Similarity
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: Clark, Hilary
: Fechtel, Kim
                                                                                                                                                    CCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGG
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TCAGGAAGCTGCTAGACGAAGGGAAGCTCTGA
                            TCAACAAAATGTTGGATGAAGAGAACATATGA 601
                                                             CGGCCCTCTATGGGCCT-----GACTTCACTCAGCACCTTGGCAAGATCTGTGACGGAC
                                                                                          CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA
                                                                                                                            CCAAGTCACATGGCCGCATCCGCCACGTGTTTGATCACTTCTCTGACCCAGGTCTGCTCA
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Resnick, Richard J.
Gulukota, Kamalakar
Graham, James R.
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Pred. No. 1.7e-43;
0; Mismatches 230
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RESULT 35
US-10-363-374-15
; Sequence 15, Application US/10363374
; Publication No. US20050048483A1
; GENERAL INFORMATION:

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RESULT 36
US-10-302-172-537
Sequence 537, Application US/10302172
Sequence 537, Application US/00302172
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Drmanac, Radoje T.
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Best Local S
Matches 336
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LOCATION: (100)...(651)
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (100)...(180)
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APPLICANT: Wang, He
TITLE OF INVENTION: NOVEL SECRETED PROTEI
FILE REFERENCE: X13020
CURRENT APPLICATION NUMBER: US/10/363,374
CURRENT FILLING DATE: 2003-02-27
NUMBER OF SEQ ID NOS: 18
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ORGANISM: Homo
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Local Similarity 58.7%;
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Pred. No. 1.7e-43;
0; Mismatches 230;
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PRIOR APPLICATION NUMBER: PCT US02/05095
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION UNMBER: US 09/799,451
PRIOR FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 950
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 537
LENGTH: 1175
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Best Local Similarity
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TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803 1CNCP
CURRENT APPLICATION NUMBER: US/10/302,172
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 10/225,251
PRIOR FILING DATE: 2002-08-20
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     636
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                                      TCAACAAATGTTGGATGAAGAGAACATATGA 601
                                                                                                CTGCCTTGTATAATCCTTTTGGGAATTTTTAAACCCCACTTACAAAAACTATGTGATGGTA 569
TCAGGAAGCTGCTAGACGAAGGGAAGCTCTGA
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Pred. No. 1.7e-43;
0; Mismatches 230;
                                                                           -GACTTCACTCAGCACCTTGGCAAGATCTGTGACGGAC
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RESULT 37
US-10-959-539-59
; Sequence 59, Application US/10959539
; Publication No. US20050048623A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.

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Best Local Similarity
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LENGTH: 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: CELL CYCLE AND PROLIFERATION PROTEINS FILE REFERENCE: PF-0722 PCT CURRENT APPLICATION NUMBER: US/10/959,539 CURRENT FILLING DATE: 2004-10-06 PRIOR APPLICATION NUMBER: US/10/031,915 PRIOR FILING DATE: 2002-01-18 PRIOR PPLICATION NUMBER: 60/145,075; 60/153,129; 60/164,647 PRIOR PRIOR DATE: 1999-07-21; 1999-09-08; 1999-11-10 NUMBER OF SEQ ID NOS: 108 SOFTWARE: PERL PROGram
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570 TCAACAAAATGTTGGATGAAGAGAACATATGA 601
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BANDMAN, Olga
AZIMZAI, Yalda
YANG, Junming
LU, Dyung Aina M.
BAUGHN, Mariah R.
PATTERSON, Chandra
                                                                                       CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA 569
                                                                                                                                                            CCAAGTCACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTGG
                                                                                                                                                                                             CTGGCCTGCTGACCGAGTGCCGGGATGTGCTGCTAGAGTTGGTGGAACACCACCTCACGC
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Pred. No. 1.8e-43;
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APPLICANT: Hypeq, Inc.
APPLICANT: Hypeq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENTITIES OF INVENTION: PROM VARIOUS CDNA LIBRAL
FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 35521
LENGTH: 422
TYPE: DNA
TYPE: DNA
TYPE: DNA
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                                                                                 ; ORGANISM: Homo sapiens
US-09-918-995-35521
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US-10-029-386-9211
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APPLICANT: Penn, Sharron G.
APPLICANT: Renk, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL, DAVID K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
Query Match
Best Local Similarity
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Best Local Similarity
Matches 169; Conserv
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.4
OTHER INFORMATION: EXPRESSED IN FEATL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
OTHER INFORMATION: EXT_HUMAN HIT: BG178783.1, EVALUE 0.00e+00
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ORGANISM: Homo sapiens
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  21.4%;
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  Score 128.4; DB 10; Pred. No. 1.1e-27;
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Pred. No. 1.2e-39;
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CDNA LIBRARIES
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CURRENT APPLICATION NUMBER: US/10/972,079; CURRENT FILING DATE: 2004-10-22; PRIOR APPLICATION NUMBER: US 60/514,333; PRIOR FILING DATE: 2003-10-24; NUMBER OF SEQ ID NOS: 96631; SOFTWARE: PatentIN version 3.1; SEQ ID NO 232; LENGTH: 565; TYPE: DNA; ORGANISM: Chicken 19866894084041_1
US-10-972-079-232
RESULT 41
US-10-191-803-330/c
; Sequence 330, Application US/10191803
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US-10-972-079-232
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Best Local
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APPLICANT: HOLM, Tom
TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-BEEF
TITLE OF INVENTION: LIVESTOCK
FILE REFERENCE: MMILLIO-2
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                                                                                                                                                                                                                                                                                                                                                                              88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
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                                                                                                                                                                                                                                                                                                               GATCCTGAGTAAAATGGCAACCAAAACCATGGCTAACATGCTCATCGATGACACGAGCAG
                                                                                                                                                                                                                                                                                                                                                                           GATCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCCGATGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGCCATGACGGCACTTAGCTTTGGTGAGGTAGACTTCACCTTCGA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGCTATGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTCCTTTGGCCCCAGTGAGCTGGCCCTGGCTACCCGCTTTCGCCAGAAGCTGCGGCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAAGATCATCAAGAACCTCAATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGTGCTAGATGAGCTCTACCGTGTGTCCAAGGAGTACACGCACAGCCGGCCCCAGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGTGCTGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACTGAGTAAGATGGCGGGTCGCTCTGTGGCTCATCTTCATAGATGAGACAAGCAGTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGGGTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACACAAGTAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCAGGACCCATGGAGTCCTTCAGCTCAAAGAGCCTGGCACTGCAAGCAGAGAAGAAGC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCCGATGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGA 89
                                                                                                                                                                              CGAAATCTTTGATGAGCTGTACAAGGTGACAAAGGAACACACAGAAACAAAA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCTGAAACAGGTCCCGATTGTTTCAGTTCCAAGAATCTTGCACTGCAAGCCCCAGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ROSENFELD, David
KERR, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 81.8; DB 22;
Pred. No. 1.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  149
                                                                                                                                                                                                                                                                                                                                                                              147
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                           APPLICANT: Algate, Alexander
APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAC
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILTE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,99
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-29
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/200,094
PRIOR PILING DATE: 2000-05-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CASTLE, Arthur

APPLICANT: ELASHOFF, Michael

TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling

FILE REFERENCE: 44921-5090US

CURRENT APPLICATION NUMBER: US/10/191,803

CURRENT FILING DATE: 2002-07-10

PRIOR APPLICATION NUMBER: US 60/303,819

PRIOR FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US 60/305,623

PRIOR APPLICATION NUMBER: US 60/369,351

PRIOR FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: US 60/369,351

PRIOR APPLICATION NUMBER: US 60/377,611

PRIOR APPLICATION NUMBER: US 60/377,611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 42
US-09-796-692-4917/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MENDRICK,
APPLICANT: PORTER, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. SEQ ID NO 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4917, Application US/09796692 Publication No. US20020198362A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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NUMBER OF SEQ ID NOS: 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCCTTGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAACAAAATGTTGGATGAAGAGAACATATGA 601
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HIGGS, Brandon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%;
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Pred. No. 7.3e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4917, Application US/10040862 Publication No. US20030078396A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version SEQ ID NO 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Mention, Jane
APPLICANT: Retter, Marc
APPLICANT: Corixa Corporation
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -10-040-862-4917/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/190,479 PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 9597
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LOCATION: (77)
OTHER INFORMATION: n=A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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les 63; Conserv
                                  APPLICATION NUMBER: US 60/223,416
FILING DATE: 2000-08-04
APPLICATION NUMBER: US 60/223,378
                                                                                                                                                            APPLICATION NUMBER: US 60/206,201
FILING DATE: 2000-05-22
APPLICATION NUMBER: US 60/218,950
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/200,545 FILING DATE: 2000-04-27
                                                                                                  FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
FILING DATE: 2000-08-03
                                                                                                                                                                                                                        FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/200,999
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/200,779 FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 60/200,303 FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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NUMBER: US 09/796,692
                                                                                                                                                   2000-05-22
NUMBER: US 60/218,950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-08-04
                     2000-08-07
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100.0%; Pre
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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; LOCATION: (77)
; OTHER INFORMATION: n=A,T,C
US-10-040-862-4917
                                                                                                  SOFTWARE: Fas
SEQ ID NO 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
                                                                                                                                       Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 10979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 014058-014402ŬS
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
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                                                                                                                                                                              PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therap
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaiger, Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                       TYPE: DNA
ORGANISM: Homo sapiens
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                ENGTH: 538
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                                                                                                                                                                                            APPLICATION NUMBER: US 60/218,950 FILING DATE: 2000-07-14 APPLICATION NUMBER: US 60/222,903
                                                                                                                                                                                                                                                                                           FILING DATE: 2000-05-01
APPLICATION NUMBER: US 60/202,084
FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/200,999
                                                                                                                                                                                                                                                        FILING DATE: 2000-05-22
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/206,201
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                                                                                                                     FastSEQ for Windows Version 3.0
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Corixa Corporation
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Clapper, Jonathan
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tive 0;
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Pred. No.
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                                                                                                                                                            File
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                                                                                                                                                                                                    ; ORGANISM: Homo sapiens; FEATURE; NAME/KEY: misc feature; LOCATION: (1)...(538); OTHER INFORMATION: n = g, a, c or t US-10-154-884B-4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-154-884B-4917/c
Sequence 4917, Application US/10154884B
Publication No. US20040005561A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = g, a, c
US-10-057-475B-4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR PRIOR DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR PRIOR PAPPLICATION NUMBER: US 60/200,545
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-27
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-04-28
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR PILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-04
PRIOR PILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/208,203
PRIOR APPLICATION NUMBER: US 60/208,203
PRIOR PILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
PRIOR PILING DATE: 2000-08-03
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                                                                                                                           Query Match
Best Local Similarity
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LENGTH: 538
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                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc W.
APPLICANT: Coriax Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013521US
                                                                                                                                                                                                                                                                                                                                                                                                                                 Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 11290 SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
599 TGA 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     478 TGA 476
                                                                                              10.5%; Score 63; DB 17; 1 ilarity 100.0%; Pred. No. 5.6e-08; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See File Wrapper or PALM
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                                                                                                 Gaps ·
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Qy 599 TGA 601
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Db 478 TGA 476
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Search completed: July 28, 2005, 19:13:31 Job time : 593 secs

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 100
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Match
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601
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      EST:*
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gb_est6: *
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      GenCore version 5.1.6 (c) 1993 - 2005 Compugen
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    CP593784
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CN305329
CB990165
BQ424670
B1752550
CN305327
AL54527566
BN91922
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AL527566
EN91923
CR611795
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BQ424670 AGENCOURT
B1752550 603021969
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CD521721 AGENCOURT
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REFERENCE
AUTHORS
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KEYWORDS
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Best Local Similarity
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Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) w.
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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AGENCOURT 15624053 NIH MGC_147 Homo
IMAGE:30528465 5', mRNĀ sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                   CTTCAGCGTCCCGGCGCCGCCACACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                                                                                                                                CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
                                                          AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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Location/Qualifiers
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fwAGE:30528465"
/tissue_type="Human Placenta"
/lab_host="DH10B_TonA"
                                                                                                                                                                                                                                                                                                                    /Clone lib="NIH MGC_147"
//note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This
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Pred. No. 3.9e-152;
0; Mismatches 1;
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sapiens cDNA clone
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AUTHORS
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CF272384
CF272384.1 GI:33628296
EST.
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1 (bases 1 to 920)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                    http://image.llnl.gov
Plate: NDAM573 row: m column:
                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                           National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
                                                                                                                                                                                                                                                                                                                                                                              Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
/clone="IMAGE:30512832"
/tissue_type="Brain glioblastoma"
/lab_host="DH10B (T1 phage-resistant)"
                                                        /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Fisk, G.J.,

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Query Match
Best Local Similarity
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/note="Vector: pExpress1; Site_1: SmaI; Site_2: NotI;
library was constructed by reverse transcription of 1
mRNA using the oligo dT primer GCGGCCGCC(7)20 and an
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Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 737 Std Error: 0.00.
Location/Qualifiers
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Contact: Brandenberger R
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CN305329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geron Corporation
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                           TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTTCCATCAGG
                                                                                                                                                                                    TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                                                                                                                                                                                                                    TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGAIGAGCTAGCATTGA
                                                                                                                                                                                                                                                                             GGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                                                                                                                                                                                            GGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                                                                                                                                                                                                                                           CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
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                                                                                           TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GRM_PREHEP"
/note="oligo dT_primed, full-length enriched cDNA library
from DMSO-treated hBS cell line H9 (p22) maintained in
feeder-free conditions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue_type="embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:47321743
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99.5%;
  TTGACCGGAATGTGTTATCCAGGCTGTTAAATGAATGCAGAGAGATGC
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Pred. No. 1.1e-151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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GA 664

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423 360 363 300 303 240 243 180 183 120 123 60 63 \vdash

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TITLE
                                                                                                                                          Query Match
Best Local Similarity
Matches 599; Conserv
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                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB990165
CB990165.1 GI:30284685
EST.
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High quality sequence stop: 635.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 780)
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AGENCOURT 13902271 NIH MGC_147 Homo
IMAGE:30347855 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (human)
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AAAACCTGGCCGTTCAGGCACAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
                                                                                      CTTCAGCGTCCCGGCGCCGTCGC-CGACTCCTCCGATGGCCACAGATGTCTTTAATTCCA
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                                                                                                                                            Conservative
                                                                                                                                                                                                                              /note="Organ: placenta; Vector: pBluescriptR; Site_1:
all-XhoI; Site_2: BamH; Oligo-dT primed using primer
5'-TTTTTTTTTTTTTTVN-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIMH/NHGRI, National Institutes of Health). Note: This is
a NIH_MGC library."
                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Human Placenta"
/lab_host="DH10B TonA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone="IMAGE:30347855"
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                                                                                                                                        Score 586.8; DB 6;
Pred. No. 1.1e-151;
0; Mismatches 2;
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                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
                                                                                                                  http://image.llnl.gov
Plate: LLAM11437 row: 1 column:
High quality sequence stop: 809.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BI819214.1
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/clone="IMAGE:5175702"
/lab_host="DH10B"
                                                                            organism="Homo sapiens"
                                          db_xref="taxon:9606"
                                                                                                  .813
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                                                            _type="mRNA"
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AGENCOURT_7833747 NIH_MGC_67
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
clestroyed upon cloming). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 896)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
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AACCCCACTTACAAAAACTATGTGATGGTATCAACAAAATGTTGGATGAAGAAACATAT
                                                                                           TTGATCATTTTTCAGATTGTGAATTTTTGGCCTTGTATAATCCTTTTTGGGAATTTTA
                                                                                                                                                       TGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAATGTGT
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
Technologies."
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/db_xref="taxon:9606"
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plate: LLAM11481 row: j column: 18
High quality sequence stop: 813.
Location/Qualifiers
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Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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[ (bases 1 to 876)
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/mol_type="mRNA"
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17000532623591 GRN_ES Homo
CN305327
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Transcriptome Characterics
                                                                                                                                                                                                                                                                              Tel: 650 473 8658 Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                             Geron Corporation
230 Constitution Drive,
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Brandenberger, R., Wei, H., Zhang, S.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                              rbrandenberger@geron.com
Length: 712 Std Error:
Location/Qualifiers
                                                                        /clone lib="GRN_ES"
/notes oligo of primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"
                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                     tissue_type="embryonic stem cells,
              93.9%;
                Score 564.4; DB 7;
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                                                                                                                Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA sea digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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1 (bases 1 to 718)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Pull-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:31271310.
                                                                                                                                                                                                                                                                                                                                                                                                                           AL549492 718 bp mRNA linear AL549492 Homo sapiens PLACENTA COT 25-NORMALIZED F CLONE CSODIO44YG13 5-PRIME, mRNA sequence.
AL549492 AL549492 GI:45749887 EST.
                                                  For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO44ADO7QPl&c=3485.f. Location/Qualifiers
                                                                                                                                                                                                                     Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                                                                                                                                                                                                                                                      Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                             Homo
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/organism="Homo sapiens'
/mol_type="mRNA"
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/clone="CSODI044YG13"
/tissue type="piAcENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
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IMAGE:304T3002 5', mRNA sequence.
CD521721
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collec Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
                                                                                                                                                                   Homo sapiens
Office of Cancer Genomics
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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High quality sequence stop: 603.
Location/Qualifiers
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/clone lib="NIH MGC 191"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adm Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGCGCACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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/tissue_type="Pooled"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                      216 TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Feb 13, 2001 this sequence version replaced Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY ced
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL527566 897 bp mRNA linear ES AL527566 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED CDNA Clone CSODC024YA23 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODC024AA12QP1&c=3485.f.
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TTAATCAAGATGAGCTAGCATTGATGGAGGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                                                                                  GTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACACAAGTAGTGAGGTGC
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/db_xref="taxon:9606"
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Pred. No. 1.9e-145;
0; Mismatches 1;
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                       565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
plate: LLAM12776 row: d column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 1055)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AGENCOURT_6715690 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748442
5', mENA sequence.
BM919223
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 677.
Location/Qualifiers
                       Conservative
                                                                                                                 /clone libe WIH MGC 120"
/clone libe WIH MGC 120"
/note=Torgan: pooled pancreas and spleen; Vector:
/note=Torgan: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: Not1; Site 2: ECGRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcGRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                      /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo Bapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5748442"
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                                       93.9%;
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                     Score 564.4; DB 5;
Pred. No. 2e-145;
0; Mismatches 1;
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                                  Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR611795 1610 bp mRNA linear full-length cDNA clone CS0DI057YA07 of Placenta Cot of Homo sapiens (human).
                                                                                                                                                                                                                                               Faraday Avenue
2 (bases 1 to 1610)
                                                                                                                                                                                                                                                                                         http://fulllength.invitrogen.com/
                                                                                                                                                                                                                                                                                                              Contact :
                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Feng Liang Email :
                                                                                                                                                                                                                                                                                      fliang@lifetech.com URL : .com/ InVitroGen Corporation 1600
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                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1733)
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 Faraday Avenue
2 (bases 1 to
                      Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                          CR615621
CR615621.1 GI:50496428
HTC; CNSLT_CDNA.
                                                                                                                                                                            CR615621 1733 bp mRNA linear | full-length cDNA clone CSODC024YA23 of Neuroblastoma 25-normalized of Homo sapiens (human).
                                             Unpublished
                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                             Homo sapiens (human)
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSUDIO57YA07"
/tissue_type="Placenta Co-
/plasmid="pCMVSPORT_6"
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Pred. No. 2.
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TITLE
JOURNAL
CR615131
full-length cDNA clone Clof Homo sapiens (human).
CR615131
CR615131.1 GI:50495938
HTC; CNSLT_cDNA.
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Query Match
Best Local Similarity
Matches 565; Conserv
541
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Direct Submitsion

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr -

- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                     AAATGTTGGATGAAGAGAACATATGA
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AAATGTTGGATGAAGAGAACATATGA
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOUCO24YA33"
/tissue_type="Neuroblastoma_C
/plasmid="pCMVSPORT_6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       division of Invitrogen
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BP 191 91006 EVRY cedex - FRANCE (5-mail : segref@genos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hon

1 (bases 1 to 1754)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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Pred. No. 2.2e-145;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IST STRAND CDNA WAS primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 1485 f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL550457 Homo sapiens PLACENTA (
Clone CSODIO57YAO7 5-PRIME, mRN/
AL550457
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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Li,W.B., Gruber,C.,
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                                                                                       TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTTAAGAAGAAGTTCATCAGCTTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="PIACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/clone="CS0DI057YA07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 562.8; DB 1;
Pred. No. 5.2e-145;
0; Mismatches 2;
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3485.
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AL554168
AL554168.3 GI:45858929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.genoscope.cns.fr/cdna?s=CS0DI081AH06QP1&c=3485.f.
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AL554168 Homo sapiens PLACENTA
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    GTAAAATGGTGTCCAAATCCATCGCCACCATCATAATAGACGACAAAGTGGTGAGGTGC
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-cligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI081Y011"
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99.5%;
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Pred. No. 7e-145;
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AGENCOURT 13618130 NIH MGC 148 Homo sapiens
IMAGE:30337918 5', mRNA sequence.
CB991862
                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with l
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Plate: NDAM363 row: 1 column: 23
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/db_xref="taxon:9606"
/clone="IMAGE:30337918"
/note="Organ: placenta; Vector:
all-xhol; Site_2: BamH; Library
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Mammalia; Eutheria; Primates; Ca
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Full-length cDNA libraries and r
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Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGATCATTTTCAGATTGTGAATTTTTGGCTGCCTTGTATAATCCTTTTGGGAATTTTA
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                                                                                                                                               sapiens
                                                                                                                                                             sapiens (human)
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                                                                                                                                                                                                                           Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE013YJ17 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              directionally cloned using primer $'-TTTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-lenght clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC
                                                                                                                                                                                                GI:45718495
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Pred. No. 2.3e-144;
0; Mismatches 1;
                     version replaced
                                                                          and Polayes,
                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                        normalization
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                     gi:30548565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Interest of the CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies, a was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence belongs to sequence cluster 3485.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE013CE09QP1&c=3485.f. Location/Qualifiers
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                         AAATGTTGGATGAAGAGAACATATGA
                                                                                                    TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                                                                                                             CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                                                                                                                          TGTTAAATGAATGCAGAGAGAGGTGCACCAAATCATTCAGCGCCCACCTCACTGCCAAGT
                                                                                                                                                                                                                                                                                                                    TGACCGTGGTCAGTTTCCATCAGGTGGATWATACCTTTGACCGGAATGTGTWATCCAGGC
                                                                                                                                                                                                                                                                                                                                       TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTTATCCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                   TTAATCAARATGAGCTAGCATTGATGGARAAATTTAARAAGAAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                        TTAATCAAGATGAGCTAGCATTGATGAGGAAATTTAAGAAGAAGTTCATCAGCTTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /Clone="Couper_TATE |
/tissue_type="placenta"
/tissue_type="placenta"
/clone_Tib="Homo sapiens PLACENTA"
/clone_Tib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned : the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapier
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE013YJ17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.8%;
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Pred. No. 1:1e-143;
2; Mismatches 2;
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DEFINITION
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Best Local S
Matches 560
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKF2p469E1232) is available the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR548728
CR548728.1 GI:50242352
EST.
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DKFZp469E1232_r1 469 (synonym: pkid1)

DKFZp49E1232_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz.heidelberg.de; sequenced by Olagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Fobo,G., Han,M. and Wiemann,S. Pongo pygmaeus mRNA (Bahr,A., Lauber,J., Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pongo pygmaeus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 779)
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                                                                                     TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                                                                                                                                                                        TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGGCAGAGAAGA
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                                                                                                                                                               TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
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                                                                                                                                                                                                                                                                                                                                                          GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACGAGTAGTGAGGTGC
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                                                                                                                                       TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                             TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                                                                                                                                                                                     TGGATGAGCTCTACAGAGTGACCAGGGAGTACACTCAAAACAAGAAGGAGGCAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="DKFZp469E1232"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 556.4; DB 7;
Pred. No. 3e-143;
0; Mismatches 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283006. Contact: Genoscope
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AL558873 Homo sapiens T
Homo sapiens cDNA clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSDJ015YH94"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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                                                                                                                                                                                                                                                                                                     92.3%;
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Pred. No. 8.8e-143;
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                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11457 row: k column: 04
High quality sequence start: 5
High quality sequence stop: 869.
                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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EST.
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603042814F1 NIH_MGC_116
                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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BI759027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens (human)
          /clone lib="NIH MGC 116"
/note="Organ: pooled colon, kidney, stomach; Vector:
/note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-SpORTG; Site 1: Not1; Site 2: BCORV (destroyed);
source anonymous pool of 3 colons, age 26 yo male, 49
female, 71 yo male colon; 46 yo male kidney, and pool
stomachs, 62 yo male and 70 yo female Library is
oligo-dT primed and directionally cloned (EcoRV site
destroyed upon cloning).
                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5183355"
                                                                                                                                                                      organism="Homo
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Similarity
CACATGGACGGGTTAATAATGTGTTTGATCATTTTTCAGATTGTGAA-TTTTGGCTGCCT
                       CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                     TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                   TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                                                                                           TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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998 bp mRNA linear EST 13-MAY-2004
ILLUMIGEN MCQ_30108 Katze MMPB Macaca mulatta cDNA clone IBIUW:6795
5' similar to Bases 72.to 998 highly similar to human TNFAIP8
(Hs.17839), mRNA sequence.
CN648259
CN648259.1 GI:47161702
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecidae; Macaca.

1 (bases 1 to 998)

1 (Ratze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L. Large-scale Rhesus Macaque cDNA Sequencing Unpublished (2003)

1 (Contact: C. Magness Illumigen Biosciences Inc. 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA Tel: 2063780400
                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta
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BACKWARD: CACTATAGGGCGAATTGGGTA
Insert Length: 998 Std Error: 0.00
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                                                TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCAACA
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AAATGTTGGATGAAGAGAACATATGA
                                                                                                                  CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                              TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGTCACCTCACTGCCAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="adult"
//ab_fitse="E. coli SOLR"
//ab_host="E. coli SOLR"
//clone lib="Katze MMPB"
/note="Vector: Uni-ZAP XR; Site_1: EcoR I; Site_2: Xho I
Created from Stratagene ZAP-cDNA Synthesis kit (Gatalog #200400) and ZAP-CDNA Gigapack III Gold Cloning Kit
(Catalog #200450)"
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/cell_type="PBMC"
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/strain="Indian"
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Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chi
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                                                                                                                                                                              562;
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRI human cDNA project 
Unpublished (2000)
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 816)
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TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCCACCTCACTGCCAAGT
                                                       TGACCGTGGTCAGTTTCCAGCGGGGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="PLACE1001920"
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/note="Vector: pME18SFL3"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 580)
Chirota M. Sakakibara, Y., Chiba, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Virology
Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jag Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
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                                                                                                    ATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCA
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Sugano cDNA library,
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/mol_type="mRNA"
/db_xref="taxon:9606"
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|e_lib="Sugano cDNA library, macrophage'
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                            Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 461.
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Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              /note=Torgan: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDMA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@ingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                         /tissue_type="Purified pancreatic islet"
/lab_host="DH108"
/clome lib="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescr:
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'db_xref="taxon:9606"
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 Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCRVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                     BX405197 834 bp mRNA
BX405197 Homo sapiens T CELLS (JURKAT CELL
clone CS0DH001YB17 5-PRIME, mRNA sequence.
                                                                                                                   On May 15, 2003 this sequence version replaced gi:30762567. Contact: Genoscope
                                                                                                                                                   Li, W.B., Gruber, C., Jessee, Full-length cDNA libraries
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 834)
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BX405197.2
                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                    Homo sapiens (human)
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         AGENCOURT 14360208 NIH MGC_191 Homo sapiens IMAGE:30410510 5', mRNA sequence. CD520304 CD520304.1 GI:31452022 EST. Homo sapiens (human)
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/db xref="taxon:9606"
/clone="CSODH001YB17"
/clsue_type="T CELLS (JURKAT CELL LINE)
/cell_line="JURKAT CELL LINE"
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Pred. No. 2.7e-138;
5; Mismatches 9;
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Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E: Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDCM200 row: m column: 15
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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TGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
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/tissue_type="Pooled"
/tissue_type="Pooled"
/lab_host="DH10B (TI phage-resistant)"
/clone lib="WIH MGC_191"
/clone lib="WIH MGC_191"
/clone lib="WIH MGC_191"
/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgctcggcc); Library is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA adn Ionomycin. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
5'-CATGCGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGCGGCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.69 kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3e-138;
0; Mismatches 16;
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                                                                                                                                                                                           146
 326
                                276
                                                                                 216 TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                              206 TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGA
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                                                                                                                                                                                                                           96 GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                                                36 TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAAGATCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun Yat-sen University
651 DongFeng Road East,
Tel: 86-1380-9770-743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD701806 622 bp mRNA linear EST 25-CEST18330 human nasopharynx Homo sapiens cDNA, mRNA sequence CD701806 GD:32232436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: YiXin Zeng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcriptional Gene 
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 622)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: yxzeng@gzsums.edu.cn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer Center
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                                                                                                                                                                                                                                                                                                                                              Similarity
                      TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                                TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                                                                                                                                                    GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                          TGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="normal nasopharynx"
/clone_Tib="human nasopharynx"
/oclone_Tib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA
library from southern Chinese"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                            89.4%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                          Score 537; DB 6;
Pred. No. 7e-138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GuangZhou 510060, China
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E 1 (bases 1 to 580)

Suzuki, Y. Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

L Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
                        294
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clone DMC08945, mRNA sequence
BP228279
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CATTGATGGAGAAATTTAAGAAGAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCC
                                                                                  AGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAG
                                                                                                                                                                                                                                        CCATCGCCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAG
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                                                         AGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAG
                                                                                                                                   TGACCAGGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCA
                                                                                                                                                            TGACCAGGGAGTACACCCAAAACAAGAAGGAGGAGAGAAGATCATCAAGAACCTCATCA
                                                                                                                                                                                                        CCATCGCCACCACCTTAATAGACGACACAAGTAGTGGGGTGCTGGATGAGCTCTACAGAG
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                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="DMC08945"
/clone_lib="Sugano cDNA library, dermoid cancer"
/note="dermoid cancer"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                       Score 535; DB 5;
Pred. No. 2.5e-137;
0; Mismatches 1;
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dermoid cancer Homo sapiens cDNA
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Best Local Similarity
Matches 569; Conserv
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60 AAAACCTGGCCGTTCAGGCACAAAAGAAGTCTTGGGTAAAATGGTGTGCCAAATCCATCG
                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, I. Lebkowski, J and Steatton, L.W.

Transcriptome characterization elucidates signaling net control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004)

Contact: Brandenberger R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 650 473 8658
Fax: 650 473 7760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geron Corporation
230 Constitution Drive,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          rbrandenberger@geron.c
Length: 672 Std Erro
Location/Qualifiers
                                                                                                                                                                                                                     /tissue type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7" /clone lib="GRN PRENEU" /note="oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic and mitogens."
                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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                 FORWARD: ATGCACTCCGAAGCAGAAGAATCCAA
BACKWARD: CATATGTTCTTCATCCACCATTT
INSET Length: 566 Std Error: 21.00
Plate: 11075 row: 05 column: F
Seq primer: ACTGGCCGTCGTTTACAACGTCGTGACTGGGAAAAC
High quality sequence start: 104
                                                                                                                                                                                                                       Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, F
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                         Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O., Clinglingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T., Simmons,B., Sequerra,R., Bosak,S., Osciette-Stamm,L., Peuch,C., Vandenhaute,J., Cusick,M.E., Albala,J.S., Hill,D.E. and Vidal,M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics Genome Res. (2004) In press
                                                                                                                                                                 Email: Marc_Vidal@dfci.harvard.edu

ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned results from a PCR_reaction_using an MGC full-length cDNA as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CV023086 566 bp mRNA linear EST 20-AU 5463 Full Length cDNA from the Mammalian Gene Collection Homo sapiens cDNA 5' similar to BC007014, mRNA sequence.
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1 (bases 1 to 566)
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quality sequence stop: 565
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                                                                                                                                                              DKFZp469E2119_r1 469 (synonym: DKFZp469E2119_5', mRNA sequence CR557522
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (bases 1 to 707)
                                                                                Pongo pygmaeus (orangutan)
Pongo pygmaeus
                                                                                                                                             CR557522.1 GI:50278801
    Poustka,A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="mixed"
/clone_Tib="Full Length cDNA from the Mammalian
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/mol_type="mRNA"
/db_xref="taxon:9606"
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  Albert, R., Moosmayer, P.,
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Pred. No. 6.8e-137;
0; Mismatches 1;
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Schupp, I.,
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Best Local Similarity
Matches 533; Conserv
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Wiemann,S.
Pongo pygmaeus mRNA (
Unpublished (2004)
Contact: MIPS
MIPS
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  ir55c03.x5
similar to
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http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFzp469E2119
Further information about the clone and the sequencing project in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; any. Please contact RZPD for
                             CK903031
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                                                                                                                 TGTATAATCCTTTTGGGAATTTTAAACCCCACTTACAAAAACTATGTGATGGTATCA
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/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
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Location/Qualifiers
572 bp mRNA linear EST 11-MAR-2004
HR85 islet Homo sapiens cDNA clone IMAGE:6548934 3'
TR:095379 095379 MDC-3.13 ISOFORM 2. [2] TR:Q9UP47 ;,
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Pred. No. 4.3e-136;
0; Mismatches 4;
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AUTHORS
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CK903031
CK903031.1 GI
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                                                                                                                                                                                                                                                                                    Similarity
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MA 02138
MA 02138
Tel: 617-495-1812
Tes: 617-495-8557
Fax: 617-495-8557
Rmail: dmelton@biohp.harvard.ed
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Harvard University, Howard Hughes Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 572)

Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Other_ESTs: ir55c03.y1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Possible reversed clone: similarity Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Good hit to opposite strand read. .. MOUSE-PANCREAS VERIFICATION
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                                                                                                     GGGAGTACACCCAAAACAAGAAGGAGGGGAGAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                                                                                                                                                                            AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                                                                             GGGAGTACACCCAAAACAAGAAGGAGGCAGAGAAGATCATCAAGAACCTCATCAAGACAG
                                                                                                                                                                             CCACCACCTTAATAGACGACACAAGTAGTGAGGAGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                          CCACCACCTTAATAGACGACACAAGTAGTGAGGTGCTGGATGAGCTCTACAGAGTGACCA
                                                                                                                                                                                                                                                                             AAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGGGTAAAATGGTGTCCAAATCCATCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=Torgan: Pancreas; Vector: pBluescript SK(-); Site 1: Noti; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Mashington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@lingate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:6548934"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens
/mol_type="mRNA"
/db_xref="taxon:9606"
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TITLE
JOURNAL
COMMENT
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AV713586
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Best Local S
Matches 533
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                       96
                                                                          36
                                                                                                      533;
                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, 1
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 697)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.; Lu,G., Cheng,Z. and Han,Z.

Lu,G., Cheng,Z. and Han,Z.

Homo sapiens CDNA, DCB clones
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AV713586 DCB Homo sapier
AV713586
AV713586.1 GI:10795103
                                                                                                                                                                                                                                                                                                                                         Fax: 86-21-50801922
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                                                                                                                Similarity
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                                                             TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCCCACTTACAAAAA 556
              GTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACACAAGTAGTGAGGTGC
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                                               TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens
                                                                                                                                                                                                                                                                                               hanzg@chgc.sh.cn
lone is available at CHGC
Location/Qualifiers
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                                                                                                                                                             /note="Vector: pTriplEx2; Site_1:
                                                                                                                                                                                          /cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DCBBBB11"
                                                                                                                                                                                                                                                                                      . 697
                                                                                                              88.1%;
                                                                                                                                                                               lib="DCB"
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Pred. No. 9.3e-136;
0; Mismatches 6;
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336 TGACCGTGGTCAGTTTTCCATCAGGTGGATTATACCTTTTGACCGGAATGTTGTTATTCCAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 739)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BG434534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        602506586F1 NIH_MGC_79 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       quality sequence stop:
Location/Qualifiers
/organism="Homo sapiens"
/mol type="mrNA"
/mb xref="taxon:9606"
/db xref="taxon:9606"
/clome="IMAGE:4603917"
/clome="IMAGE:4603917"
/lab host="DH10B (T1 phage-resistant)"
/lab host="DH10B (T1 phage-resistant)"
/clome=lib="NIH MGC_79"
/clome_lib="NIH MGC_79"
/site_1: Sfil (ggccgtctggcc); Site_2: Sfil
(ggccgtttatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.3
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
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RESULT 37
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Pongo pygmaeus mRNA
Unpublished (2004)
Contact: MIPS
                                                                                                                                                                                 DKFZp469I0535_r1 469 (synonym: DKFZp469I0535_5', mRNA sequence
                                                Poustka,A., Albert,R., Moosmayer,P.,
Mewes,H.W., Weil,B., Amid,C., Osange
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                 Pongo pygmaeus (orangutan)
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No. 3e-135;
                                                yer,P., Schupp,I., We
Osanger,A., Fobo,G.,
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                        Albert, R., Moosmayer, P.,
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G., Han,M. and
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BG534704 685 bp m 602553867F1 NIH MGC_77 Homo sapiens mRNA sequence.
BG534704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp46910535 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
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/mol type="mRNA"
/db_xref="taxon:9600"
/clone="bKrZpA6910535"
/tissue_type="kidney"
/dev stage="adult"
/lab_host="DH10Br
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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GATGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGTCACATGGACGGGTTAATAA
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/lab host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/clone_lib="NIH_MGC_77"
/clone_lib="NIH_MGC_77"
/clone="Organ: lung; Vector: pDNR-LIB (Clontech); Site 1:
/note="Organ: lung; Vector: pDNR-LIB (Clontech); 5<sup>7</sup> and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCAATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCCGACACGCGCCAATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 4.3e-133;
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                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: High quality sequence stop: !
                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 593
Plate: 11028 row:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Marc_Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry c
results from a PCR reaction using an MGC
template DNA and ORF specific primers
PCR_PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 593)
Rual(Dases I Hrozane-Kishikawa,T., Hao,T., Bertin,N., Li,S., Prioc. N., Vi
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Fax: 617 632 5739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                 /note="Vector: mixed; The ORFs were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway Coloning into pDONR223 Donor vector. Reference: MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences: PNAS,
                                                                                                                                                                 Collection"
                                                                                                                                                                             /organism="Homo sapiens"
/mol type="mrNA"
/mol type="mrNA"
/db xref="traxon:9606"
/tissue_type="mixed"
/clone_Tib="Full Length cDNA from the Mammalian Gene
                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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C full-length cDNA as
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Query Match Best Local Similarity Matches 547; Conserv

Conservative

98.0%;

Score 519.2; DB 7; Pred. No. 6.1e-133; 0; Mismatches 8;

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AUTHORS
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                                                                                                                                   Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tisse Procurement: Narayan Bhat
            CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDCM200 row: k column: 07 High quality sequence stop: 563.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CD520319.1 GI:31452037
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CD723203 588 bp
0j19b07.yl Human lacrimal gland,
clone 0j19b07 5', mRNA sequence.
CD723203
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98.7%;
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TGTATAATCCTTTTGGG--AATTTTAAACCCCACTTACAAAAACTATGTGA-TGGTATCA
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/tlissue_type="Pooled"
/tlissue_type="Pooled"
/lab_most="PullOB (TI phage-resistant)"
/clone_lib="NIH_MGC_191"
/clone_lib="NIH_MGC_191"
/clone_lib="NIH_MGC_191"
/clone="Yector: pDNR-LIB; Site_1: SfiI (gyccattatgycc);
/inte="Yector: pDNR-LIB; Site_1: SfiI (gyccattatgycc);
/inte="Yector: pDNR-LIB; Site_1: SfiI (gyccattatgycc);
/inte="Yector: pDNR-LIB; Site_1: SfiI (gyccattatgycc);
/inte = "Yector: pDNR-LIB; Site_1: SfiI (gyccattatgycc);
/inte = "Yector: pDNR-LIB; Site_1: SfiI (gyccattatgycc);
/inte = "Yector: policy is oligo-dT primed and directionally cloned. PBMC - Peripheral Blood and directionally clones; site_1: Site_1:
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: graeme@helix.nih.gov
Plate: 19 row: b column:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                           CAGGCTGTTAAATGAATGCAGAGAGATGCTGCACCAAATCATTCAGCGCCACCTCACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Human lacrimal gland, unamplified: oj"
/note="Organ: Eye; Vector: pCMVSport6; RNA was extracted
from 2 human lacrimal glands. A directionally cloned cDNA
library in the pCMVSPORT6 vector(Life Technologies) was
constructed at Bioserve Biotechnology (Laurel MD)
essentially following the protocols of the SuperScript
Plasmid System full details of which are contained in the
manufacturer's Instruction manual
(http://www.lifetech.com/). First strand synthesis was
carried out using a Not I primer-adapter
[5'.pGACTAGTTCTAGATCGCGAGCGGCCCCC((1)15-3']. EST analysis
was performed on the unamplified library at the NIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intramural Sequencing Center (NISC)."
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/dev_stage="Adult"
/lab_host="EMDH10B"
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/db_xref="taxon:9606"
/clone="oj19b07"
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jag
Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mizushima-Sugano,J., Nakai,K. and Sugano,S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP345938 583 h
BP345938 Sugano cDNA library,
clone SYN08154, mRNA sequence
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Suzuki,Y., Yamashita,R.,
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                                                  TGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTATGACCGTGGTCAGTTTCCATCAGG
                                                                                             TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
                                                                                                                           TCATCAAGCTGGCCATTCTTTATAGGAATAATCAGTTTAATCAAGATGAGCTAGCATTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SYN08154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="synovial membrane"
/clone_lib="Sugano cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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99.4%;
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Pred. No. 5.3e-127;
0; Mismatches 2;
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Best Local (
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                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp469M0735
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert. Clone from S Molecular Genome Analysis, German Cancer Research Center Email s.wiemann@dkfz-heidelberg.de; any. Please contact F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.

1 (Dases 1 to 605)

Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wisman, E.
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CR771295.1 GI:52614568
EST.
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Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKFZp469M0735_r1 469 (synonym: DKFZp469M0735_5', mRNA sequence
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Pongo pygmaeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MIPS
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                                                                                      TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCAAAACAAGAAGAAGGAGGAGGAAGA
                                                                                                                                      GTAAAATGGTGTCCAAATCCATCGCCACCTTAATAGACGACACGAGTAGTGAGGTGC
                                                                                                                                                                                                                                         TGGCCACAGATGTCTTTAATTCCAAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
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                                                                                                                                                                       GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC 155
                                                                                                                                                                                                           TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
                     TCATCAAGAACCTCATCAAGACAGTCATCAAGCTGGCCATTCTTTATAGGAATAATCAGT
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                           /clone="DKFZp469M0735"
/tissue_type="kidney"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="469 (synonym: pkid1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pongo pygmaeus"
/mol_type="mRNA"
/db_xref="taxon:9600"
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                                                                                                                                                                                                                                                                                              82.6%;
99.2%;
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                                                                                                                                                                                                                                                                                              Score 496.6; DB 7;
Pred. No. 1.2e-126;
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                                                                                                                                                                                                                                                                                                                DB 7;
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contact RZPD for
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National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI760235
603045171F1 NIH_MGC_116 Homo
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Plate: LLAM11463 row: m column:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Score 494.6; DB 4;
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library
Vector sequences were eliminated by and crossmatch version 0.990319
                                                            Email: huenishi@affrc.go.jp
EST project with full-length enriched cDNA libraries carried
EST project with full-length enriched cDNA libraries carried
Animal Genome Research Program (Japan) by National Institute
Agrobiological Sciences and STAFF-Institute
Single pass sequencing of clones derived from oligo-capped cl
                                                                                                                                                                                                                                                  Uenishi,H., Eguchi,T., Suzuki,K., Sawazaki,T., T
Okumura,N., Hamasima,N. and Awata,T.
PEDE (Pig EST Data Explorer): construction of a
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
Contact: Hirohide Uenishi
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BP433798
                                                                                                                                                            Fax:
                                                                                                                                                                             Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Tsukuba, Ibaraki 305-8602, Japan
Tel: +81-29-838-8627
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                                                     TGTATAATCCCTTTGGAAATTTCAAACCGCACTTACAGAAACTGTGTGATGGTATCAACA
                                                                   TGTATAATCCTTTTGGGAATTTTAAACCCCCACTTACAAAAACTATGTGATGGTATCAACA
                                                                                                           CACACGGACGGATTAACAAGGTCTTTGATCATTTTTCAGATTGTGATTTTCTTGGCCGCCT
                                                                                                                         CACATGGACGGGTTAATAATGTCTTTGATCATTTTTCAGATTGTGAATTTTTTGGCTGCCT
                                                                                                                                                            TGCTCAATGAGTGCAGAGAGCTGCTCCACCAGATCATCCAGCGTCACCTCACCGCCAAGT
                                                                                                                                                                                TGTTAAATGAATGCAGAGAGAGTGCTGCACCAAATCATTCAGCGCCACCTCACTGCCAAGT
                                                                                                                                                                                                                   TGACCGTGGTCAGTTTTCATCAGGTGGATTTCACCTTTGACCGGAATGTGCTATCCAGGC
                                                                                                                                                                                                                                           TGACCGTGGTCAGTTTCCATCAGGTGGATTATACCTTTGACCGGAATGTGTTATCCAGGC
                                                                                                                                                                                                                                                                      TTAATCAAGATGAGCTAGCATTGATGGAGAAATTTAAGAAGAAAGTTCATCAGCTTGCTA
                                                                                                                                                                                                                                                                                                                           TCATCAAAAACCTCATCAAAACAGTCATCAAGCTGGCCATTCTCTACAGGAATAATCAAT
                                                                                                                                                                                                                                                                                                                                                                                              TGGATGAGCTCTACAGAGTGACCAGGGAGTACACCCCAAAACAAGAAGGAGGCAGAGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                     GTAAAATGGTGTCCAAATCCATCGCCACCACCTTAATAGACGACACAAGTAGTGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGCCACAGATGTCTTTAATTCCAAAAACCTGGCCGTTCAGGCACAAAAGAAGATCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality bases were trimmed based on the quality values. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="LNG010079A10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="lung"
/dev_stage="adult"
/clone_lib="full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%;
91.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 489.2; DB 5;
Pred. No. 1.4e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enriched swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA library,
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                                                                              575
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